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(54) ANTIGENIC POLYPEPTIDE OF CHLAMYDIA PNEUMONIAE

(57) An antigenic polypeptide of *Chlamydia pneumoniae* comprising the polypeptide A containing the sequence of at least five consecutive amino acid residues in the polypeptide of SEQ ID NO: 1; a DNA coding for the polypeptide; a recombinant vector containing the DNA; a transformant containing the vector; a process for producing an anti-*C. pneumoniae* antibody by using the antigenic polypeptide as the antigen; methods for detecting and assaying the anti-*C. pneumoniae* antibody; the use of the antigenic polypeptide; a fused protein consisting of a dihydrofoliate reductase and an antigenic polypeptide *C. pneumoniae*, wherein the polypeptide of SEQ ID NO: 14 has bound to the polypeptide A containing the sequence of at least five cons cutive amino acid residues in the polypeptide of SEQ ID NO: 1; a DNA coding for the fused protein; a recombinant vector containing the DNA; a transformant containing the vector; a process for producing an anti-*C. pneumoniae* antibody by using the fused protein as the antigen; methods for detecting and assaying the anti-*C. pneumoniae* antibody by using the fused protein as the antigen; the use of the fused protein; a probe and a primer for detecting and assaying *C. pneumoniae* genes; methods for detecting and assaying *C. pneumoniae* genes by using the probe or primer; and the use of the probe or primer.

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Description

FIELD OF THE INVENTION

The invention relates to Chlamydia pneumoniae antigenic polypeptides, fused proteins containing the polypeptides, DNAs coding therefor, recombinant vectors carrying the DNAs, transformants containing the recombinant vectors, a method for production of antibody, a method and reagents for detection and/or measurement of antibody, a method and agents for diagnosis of Chlamydia pneumoniae infections, probes and primers for detection and/or measurement of Chlamydia pneumoniae gene, and a method and reagents for detection and/or measurement of Chlamydia pneumoniae gene. The invention can be effectively used in the pharmaceutical industry, particularly in the preparation of agents for diagnosis of Chlamydia pneumoniae infections.

BACKGROUND ART

Several kinds of species are known in Chlamydia, that is, Chlamydia trachomatis, Chlamydia psittaci, Chlamydia pecorum, Chlamydia pneumoniae and the like. Chlamydia trachomatis causes trachoma, venereal lymphogranuloma, urogenital infections, inclusion conjunctivitis, neonatal pneumonia and the like. Chlamydia psittaci causes psittocosis and the like. Chlamydia pneumoniae causes respiratory infections, atypical pneumonia and the like.

Since the symptoms of infections in the respiratory apparatus which are caused by Chlamydia pneumoniae are similar to those of infections caused by Mycoplasma pneumoniae or Influenza virus, physicians often make a wrong diagnosis. Hence, there is a need for the development of a simple method for diagnosing the infections caused by Chlamydia pneumoniae.

In general, an infection can reliably be diagnosed by detecting the causative bacterium in the infected site or by detecting an antibody against the causative bacterium in body fluids such as a sera and the like. The former method is called an antigen test and the latter is called an antibody test. Both of them are clinically important. As for Chlamydia pneumoniae, there is known an antibody test which is carried out by a method in which an antibody is detected by using an elementary body of Chlamydia pneumoniae.

However, this method has the disadvantage that the elementary body of Chlamydia pneumoniae reacts not only with an antibody against Chlamydia pneumoniae but also with antibodies against other species of Chlamydia, thus being fairly unspecific. This is because the elementary body of Chlamydia pneumoniae contains an antigen which is also present in other species of geneus Chlamydia than Chlamydia pneumoniae, that is, Chlamydia trachomatis and Chlamydia psittaci.

As a plasmid which can be used for the expression of a large amount of a protein in E. coli, pBBK10MM is known (Japanese Unexamined Patent Publication No. Hei 4-117284). This plasmid can be used for the expression of a fused protein of an anti-allergic peptide with DHFR. The expressed fused protein also maintains the enzymatic activity of DHFR and can therefore be purified easily by utilizing the characteristic properties and activities of DHFR.

Genetic screening has been carried out to diagnose infections. In this screening, the presence of the gene of a microorganism to be detected in a sample is examined using nucleic acid probes and the like.

As for Chlamydia pneumoniae, there is known a genetic screening method which is carried out as disclosed in Japanese Unexamined Patent Publication No. Sho 64-500083, U.S.P. No. 5,281,518 and WO94/04549.

However, Japanese Unexamined Patent Publication No. Sho 64-500083 and U.S.P. No. 5,281,518 only disclose that a chromosomal DNA of Chlamydia pneumoniae or a DNA fragment which is obtained by cleaving the chromosomal DNA with a restriction enzyme or the like is used as a probe. The base sequences of these DNA molecules are not determined and the specificity of these probes are therefore unclear. In addition, it is difficult to determine the reaction conditions.

Although WO94/04549 discloses a method using a probe which is hybridized to ribosome RNA or DNA corresponding thereto, the specificity of these probes is not reliable because the homology of ribosomal RNA is relatively high in all organisms.

DISCLOSURE OF THE INVENTION

It is an object of the invention to provide antigenic polypeptides that do not react with antibodies against species of geneus Chlamydia other than Chlamydia pneumoniae, such as Chlamydia trachomatis, Chlamydia psittaci and the like and which react only with a Chlamydia pneumoniae-specific antibody and can thereby detect the Chlamydia pneumoniae-specific antibody.

Another object of the invention is to provide a method for synth sizing large amounts of the antigenic polypeptides by using gene recombination techniques.

A further object of the invention is to provide a method for production of an anti-Chlamydia pneumoniae-specific antibody, a method and reagents for detection and/or measurement of the anti-Chlamydia pneumoniae-specific anti-

body, and agents for diagnosis of Chlamydia pneumoniae infections, all by using said antigenic polypeptides.

A still further object of the invention is to provide probes and primers for detecting and/or measuring specifically Chlamydia pneumoniae gene, a method and reagents for detection and/or measurement of Chlamydia pneumoniae gene and agents for diagnosis of Chlamydia pneumoniae infections, all by using the probes or primers.

An even further object of the invention is to provide antigenic polypeptides for detection of an antibody which reacts with geneus Chlamydia including Chlamydia pneumoniae, Chlamydia trachomatis, Chlamydia psittaci and the like.

SUMMARY OF THE INVENTION

The subject matters of the invention are as follows:

(1) A Chlamydia pneumoniae antigenic polypeptide, which comprises polypeptide containing a sequence of at least 5 consecutive amino acids in the polypeptide of SEQ ID NO: 1 (hereinafter referred to as "polypeptide A").
(2) The antigenic polypeptide of (1), wherein said polypeptide A is a polypeptide in which at least one amino acid is deleted from the polypeptide of SEQ ID NO: 1.
(3) The antigenic polypeptide of (1), wherein said polypeptide A is a polypeptide in which at least one amino acid in the polypeptide of SEQ ID NO: 1 is replaced with other amino acid or a polypeptide in which at least one amino acid is added in the polypeptide of SEQ ID NO: 1.
(4) The antigenic polypeptide of (1), wherein said polypeptide A is a polypeptide in which an amino acid or a peptide sequence is bound to a sequence of at least 5 consecutive amino acids in the polypeptide of SEQ ID NO: 1.
(5) The antigenic polypeptide of (1), wherein said polypeptide A is a polypeptide containing the amino acid sequence of SEQ ID NO: 1.
(6) The antigenic polypeptide of (1), wherein said polypeptide A is a polypeptide containing the amino acid sequence of SEQ ID NO: 2.
(7) The antigenic polypeptide of (1), wherein said polypeptide A is a polypeptide containing the amino acid sequence of SEQ ID NO: 5.
(8) A DNA encoding the antigenic polypeptide of any one of (1)-(7), or a DNA complementary thereto.
(9) The DNA of (8), which contains the base sequence of SEQ ID NO: 3.
(10) The DNA of (8), which contains the base sequence of SEQ ID NO: 4.
(11) The DNA of (8), which contains the base sequence of SEQ ID NO: 7.
(12) A recombinant vector carrying the DNA of any one of (8)-(11).
(13) The recombinant vector of (12), which is plasmid pCPN533 α containing the base sequence of SEQ ID NO: 10.
(14) A transformant containing the recombinant vector of (12) or (13).
(15) A method for production of an anti-Chlamydia pneumoniae antibody, wherein the antigenic polypeptide of any one of (1)-(7) is used as an antigen.
(16) A method for detection and/or measurement of an anti-Chlamydia pneumoniae antibody, wherein the antigenic polypeptide of any one of (1)-(7) is used as an antigen.
(17) A reagent for detection and/or measurement of an anti-Chlamydia pneumoniae antibody, which comprises the antigenic polypeptide of any one of (1)-(7) as an antigen.
(18) A reagent for diagnosis of a Chlamydia pneumoniae infection, which comprises the antigenic polypeptide of any one of (1)-(7) as an active ingredient.
(19) A fused protein of a Chlamydia pneumoniae antigenic polypeptide with dihydrofolate reductase, in which polypeptide containing a sequence of at least 5 consecutive amino acids in the polypeptide of SEQ ID NO: 1 is bound to the polypeptide of SEQ ID NO: 14 (hereinafter referred to as "polypeptide B") either directly or via an intervening amino acid or amino acid sequence.
(20) The fused protein of (19), wherein said polypeptide B is a polypeptide in which at least one amino acid is deleted from the polypeptide of SEQ ID NO: 1.
(21) The fused protein of (19), wherein said polypeptide B is a polypeptide in which at least one amino acid in the polypeptide of SEQ ID NO: 1 is replaced with other amino acids or a polypeptide in which at least one amino acid is added in the polypeptide of SEQ ID NO: 1.
(22) The fused protein of (19), which is a polypeptide containing the amino acid sequence of SEQ ID NO: 15.
(23) The fused protein of (19), which is a polypeptide containing the amino acid sequence of SEQ ID NO: 16.
(24) A DNA encoding the fused protein of any one of (19)-(23), or a DNA complementary thereto.
(25) The DNA of (24), which contains the base sequence of SEQ ID NO: 17.
(26) The DNA of (24), which contains the base sequence of SEQ ID NO: 18.
(27) A recombinant vector carrying the DNA of any one of (24)-(26).
(28) The recombinant vector of (27), which is plasmid pCPN533T.
(29) A transformant containing the recombinant vector of (27) or (28).
(30) A method for production of an anti-Chlamydia pneumoniae antibody, wherein the fused protein of any one of

(19)-(23) is used as an antigen.

(31) A method for detection and/or measurement of an anti-Chlamydia pneumoniae antibody, wherein the fused protein of any one of (19)-(23) is used as an antigen.

(32) A reagent for detection and/or measurement of an anti-Chlamydia pneumoniae antibody, which comprises the fused protein of any one of (19)-(23) as an antigen.

(33) A reagent for diagnosis of a Chlamydia pneumoniae infection, which comprises the fused protein of any one of (19)-(23) as an active ingredient.

(34) A probe for detection and/or measurement of Chlamydia pneumoniae gene, which comprises any one of

(a) a DNA containing a sequence of at least 10 consecutive bases in the DNA of SEQ ID NO: 3,
(b) a DNA complementary to DNA (a), or
(c) a DNA having at least 90% homology to DNA (a) or (b).

(35) The probe of (34), which contains the base sequence of SEQ ID NO: 19.

(36) The probe of (34), which contains the base sequence of SEQ ID NO: 20.

(37) A method for detection and/or measurement of Chlamydia pneumoniae gene, characterized in that the probe of any one of (34)-(36) is used.

(38) A reagent for detection and/or measurement of Chlamydia pneumoniae gene, which comprises the probe of any one of (34)-(36).

(39) An agent for diagnosis of a Chlamydia pneumoniae infection, which comprises the probe of any one of (34)-(36) as an active ingredient.

(40) A primer for detection and/or measurement of Chlamydia pneumoniae gene, which comprises any one of

(a) a DNA containing a sequence of at least 10 consecutive bases in the DNA of SEQ ID NO: 3,
(b) a DNA complementary to DNA (a), or
(c) a DNA having at least 90% homology to DNA (a) or (b).

(41) The primer of (40), which contains the base sequence of SEQ ID NO: 19.

(42) The primer of (40), which contains the base sequence of SEQ ID NO: 20.

(43) A method for detection and/or measurement of Chlamydia pneumoniae gene, wherein the primer of any one of (40)-(42) is used.

(44) A reagent for detection and/or measurement of Chlamydia pneumoniae gene, which comprises the primer of any one of (40)-(42).

(45) A reagent for diagnosis of a Chlamydia pneumoniae infection, which comprises the primer of any one of (40)-(42) as an active ingredient.

(46) A Chlamydia pneumoniae antigenic polypeptide, which is selected from the group consisting of

(a) the polypeptide of SEQ ID NO: 5,
(b) a polypeptide in which at least one amino acid is deleted from the polypeptide of SEQ ID NO: 5,
(c) a polypeptide in which at least one amino acid in the polypeptide of SEQ ID NO: 5 is replaced with another amino acid, and
(d) a fused polypeptide of any one of (a)-(c) with another amino acid or peptide.

(47) A Chlamydia pneumoniae antigenic polypeptide, which is selected from the group consisting of

(a) the polypeptide of SEQ ID NO: 6,
(b) a polypeptide in which at least one amino acid is deleted from the polypeptide of SEQ ID NO: 6,
(c) a polypeptide in which at least one amino acid in the polypeptide of SEQ ID NO: 6 is replaced with another amino acid, and
(d) a fused polypeptide of any one of (a)-(c) with another amino acid or peptide.

(48) A DNA encoding the polypeptide of (46), or a DNA complementary thereto.

(49) A DNA encoding the polypeptide of (47), or a DNA complementary thereto.

(50) The DNA of (48), wherein said DNA encoding the polypeptide of (46) is the DNA of SEQ ID NO: 7.

(51) The DNA of (49), wherein said DNA encoding the polypeptide of (47) is the DNA of SEQ ID NO: 8.

(52) A recombinant vector carrying the DNA of any one of (48)-(51).

DETAILED DESCRIPTION OF THE INVENTION

In the specification, deoxynucleotides having only one base are referred to as "monodeoxynucleotides" and deoxynucleotides having at least two bases are referred to as "DNAs", unless otherwise indicated.

The invention will now b explained in detail.

Antigen polypeptide

The antigen polypeptide of the present invention is formed of polypeptides containing at least five continued amino acid sequences in a polypeptide of SEQ ID No. 1 (hereinafter referred to as "Polypeptide A") from the viewpoint of the minimum size in which a peptide is allowed to possess antigenicity.

Since the antigen-antibody reaction can be expected to gain in sensitivity in proportion as the length of amino acid sequence increases, the polypeptide A is appropriately formed of not less than 20, preferably not less than 100, and more preferably not less than 250 amino acids.

So long as the polypeptide A possesses the antigenicity inherent in Chlamydia pneumoniae, it tolerates the loss of amino acids (1 - 250 amino acids, for example) from the polypeptide of SEQ ID No. 1. If the number of missing amino acids is unduly large, the polypeptide A will tend to suffer the antigenicity inherent in Chlamydia pnuemoniae to be impaired.

When the number of missing amino acids is large (five or more, for example), the polypeptide A prefers such missing amino acids (five or more, for example) to occur in a continued series for the sake of retaining the antigenicity of Chlamydia pneumoniae.

So long as the polypeptide A possesses the antigenicity inherent in Chlamydia pneumoniae, it tolerates the substitution of part of the amino acids (1 - 100 amino acids, for example) by other amino acids or the insertion of amino acids (1 - 100 amino acids, for example) in the polypeptide of SEQ ID No. 1. If the number of amino acids involved in the substitution or insertion is unduly large, the polypeptide A will tend to suffer the antigenicity inherent in Chlamydia pnuemoniae to be impaired. When the number of amino acids involved in the substitution or insertion is large (five or more, for example), the polypeptide A prefers the amino acids (five or more, for example) to occur in a continued series for the sake of retaining the antigenicity of Chlamydia pneumoniae. The amino acids to be involved in the substitution are preferred to possess such similar qualities as are observed in the substitution between glycine and alanine, for example.

So long as the polypeptide A possesses the antigenicity inherent in Chlamydia pneumoniae, it may be a polypeptide having amino acids or peptides ligated directly or through the medium of an intervening amino acid sequence to at least five continued amino acid sequences in the polypeptide of SEQ ID No. 1.

The peptides for the ligation are appropriately formed of not more than 1000 amino acid sequences, preferably not more than 500 amino acid sequences, and more preferably not more than 200 amino acid sequences for the sake of retaining the antigenicity inherent in Chlamydia pneumoniae.

As concrete examples of such amino acids or peptides, leucine, leucine-methionine, dihydrofolic acid reductase (DHFR), and β-galactosidase may be cited.

As concrete examples of the polypeptide A using DHFR or β-galactosidase as a peptide, DHFR-Chlamydia pneumoniae antigen polypeptide-fused protein and β-galactosidase-Chlamydia pneumoniae antigen polypeptide-fused protein may be cited. DHFR or β-galactosidase may be ligated either directly or through the medium of an intervening amino acid sequence with Chlamydia pneumoniae antigen polypeptide.

As concrete examples of the polypeptide A, the polypeptides of SEQ ID No. 1, SEQ ID No. 2, and Sequence No. 5 may be cited.

Though the intervening amino acid sequence is not defined particularly, the amino acid sequences of leucine and leucine-methionine are examples.

As concrete examples of the fused protein of the present invention, the polypeptide formed of amino acid sequences of SEQ ID No. 15 and the polypeptide formed of amino acid sequences of SEQ ID No. 16 may be cited.

Among the fused proteins cited above, the polypeptide formed of the amino acid sequences of SEQ ID No. 15 including the whole antigen polypeptide of 53 kDa of Chlamydia pneumoniae proves particularly advantageous.

The method of chemical synthesis and the method of gene recombination are available for the production of the antigen polypeptide of this invention.

The polypeptide of SEQ ID No. 1 of this invention is an antigen polypeptide formed of 488 amino acid residues as shown in the table of sequences.

The polypeptide f SEQ ID No. 2 of this invention is an antigen polypeptide formed f 271 amino acid residues as shown in the table of sequences.

The polypeptide of SEQ ID N . 5 of this invention is an antigen polypeptide formed of 259 amino acid residues as shown in the table of sequences.

Among other antigen polypeptides mentioned above, the polypeptide of SEQ ID No. 1 containing the whole antigen polypeptide of 53 kDa of Chlamydia pnuemoniae proves particularly advantageous.

Method for production of antigen polypeptide

The method of chemical synthesis and the method of gene recombination are available for the production of the antigen polypeptide of this invention.

Among the methods of chemical synthesis is counted the MAP (multiple antigen peptide) method, for example. The MAP method befits the synthesis of a peptide formed of not more than 30 amino acid sequences. This synthesis can be implemented by the use of a commercially available peptide synthesizing device.

Among the methods of gene recombination is counted a method which comprises inserting a DNA coding for the antigen polypeptide of this invention in a vector thereby constructing a recombinant vector, inserting the recombinant vector in a host thereby producing a transformant, and isolating the peptide aimed at from the transformant.

The DNA coding for the antigen polypeptide of this invention will be described afterward.

The vector may be plasmid, phage, etc.

As concrete examples of the host, Escherichia coli, Bacillus subtilis, yeast, etc. may be cited.

Now, the method for forming the transformant and the method for refining the peptide aimed at by the use of the transformant will be described in detail below.

Preparation of Recombinant Vector Carrying the DNA Encoding the Antigenic Polypeptide and Transformants Containing the Same

The λ phage obtained by screening (see infra) is already a kind of recombinant vector carrying the DNA of the invention. Additional recombinant vectors can be prepared by inserting in a known plasmid vector or phage vector the DNA encoding the Chlamydia pneumoniae antigenic polypeptide (see infra) in a conventional procedure. In this case, a linker may be used if necessary. As the known plasmid vector, pBR322, pUC18, pUC19, pBBK10MM or the like can be used. Plasmids pBR322, pUC18 and pUC19 are commercially available and pBBK10MM is described in detail in Japanse Unexamined Patent Publication No. Hei 4-117284. As the phage vector, λ gt11 phage, λ gt10 phage or the like can be used. In any case, recombinant vectors corresponding to the parent vectors used can be obtained.

The recombinant vectors carrying the DNA of the invention include plasmid pCPN533 α, 53-3S λ phage and the lik (see infra).

The obtained recombinant vector is introduced into a host to prepare a transformant. If an E. coli-derived plasmid or λ phage is used, an E. coli strain such as HB 101 can be used as a host. The host is treated to become a competent cell. A competent cell obtained by treating E. coli strain HB101 is commercially available from Takara Shuzo Co., Ltd. A method of introducing the recombinant vector into a host to prepare a transformant is described in "Molecular Cloning".

The obtained transformant is cultured to form colonies. Plasmid DNAs are obtained from each of the colonies and cleaved with an appropriate restriction enzyme. A transformant having a desired recombinant plasmid is selected according to the results of agarose gel electrophoretic analysis of the cleaved plasmid DNA. The plasmid vectors thus prepared include plasmid pCPN533 α.

Examples of the transformant thus prepared include E. coli strain HB101 containing the recombinant vector pCPN533 α.

Preparation of Recombinant Vectors Carrying the DNA Encoding Fused Protein of the Chlamydia pneumoniae Antigenic Polypeptide with DHFR and Transformants Containing the Same

The DNA molecule encoding the Chlamydia pneumoniae antigenic polypeptide (see infra) is ligated to the DNA molecule encoding DHFR (see infra) by means of a commercially available kit. In the ligation, a linker may be used if nec ssary. A DNA ligation kit (Takara Shuzo Co., Ltd) can be used as a commercially available kit. If the DNA obtained by the ligation does not have a replication origin and does not therefore function as a plasmid, the DNA is inserted in a separate plasmid vector, which may be pBR322, pUC18 or the like.

The ligated DNA is introduced into a host to prepare a transformant. If an E. coli-derived plasmid is used, an E. coli strain such as HB 101 can be used as a host. The host is treated to become a competent cell. A competent cell obtained by treating E. coli strain HB101 is commercially available from Takara Shuzo Co., Ltd. The method of introducing the ligated DNA into a host to prepare a transformant is described in "Molecular Cloning".

The obtained transformant is cultured to form colonies. Plasmid DNAs are obtained from each of the colonies and cleaved with an appropriate restriction enzyme. A transformant having a desired recombinant plasmid is selected according to th results of agarose gel electrophor tic analysis. An exampl of the plasmid vector thus prepared is plasmid pCPN533T.

An example of the transformant thus prepared is E. coli strain HB101 containing the recombinant vector pCPN533T.

The transformant is cultured by shaking an incubator containing the transfomant at an appropriate temperature in a medium that allows the transformant to grow until a sufficient amount of the desired antigenic polypeptide is accumu-

lated in the transformant. If E. coli strain HB101 containing the recombinant vectors pCPN533 α or pCPN533T ar used as a transformant, the cell is cultured while shaking in ampicillin-containing LB medium at 37 °C overnight. Subsequently, the culture is inoculated in ampicillin-containing TB medium and further cultured while shaking at 37°C overnight. A method for preparing the TB medium is described in "Molecular Cloning".

The cultured transformant is harvested by centrifugation and suspended in a buffer. The transformant is disrupted by sonication of the suspension. If the transformant is E. coli, the cell may be lysed by successively adding lysozyme and an SDS-containing buffer to the suspension.

When the polypeptide aimed at is secretory in quality, the culture broth is centrifuged to obtain the supernatant.

After the disruption of the transformant, the cell residue is removed by centrifugation, thereby obtaining the supernatant. Streptomycin sulfate is added to the supernatant. The mixture is stirred for a certain period of time and centrifuged to precipitate nucleic acids, thereby obtaining the supernatant.

This supernatant is precipitated with ammonium sulfate and centrifuged. Generally, the precipitate is recovered as the product. Since the supernatant possibly contains the peptide aimed at, the practice of sampling and analyzing the supernatant thereby confirming the presence or absence of the peptide proves advantageous.

Either the solution of the precipitate in a small amount of buffer solution or the supernatant is fractionated by liquid chromatography. The proteins contained in the fractions are blotted by the Western blotting method using a Chlamydia pneumoniae-specific monoclonal antibody to obtain the fractions containing antigen polypeptide. When the polypeptide A is a protein fused with DHFR, a Methotrexate column can be used as the column for the liquid chromatography. Specific procedures of the removal of residues such as a cell membrane and the like, the removal of DNA by addition of streptomycin sulfate, the recovery of proteins by addition of ammonium sulfate and a Western blotting method are described in "Molecular Cloning".

DNAs Encoding the Antigenic Polypeptides

In the invention, the DNA encoding the polypeptide of SEQ ID NO: 1 means DNAs selected from the group of DNAs which are obtained by translating the amino acids of the polypeptide of SEQ ID NO: 1 to triplets in accordance with the genetic code (each amino acid is assigned 1-6 sets of nucleotide sequences). This group of DNAs includes the DNA of SEQ ID NO: 3.

The DNA encoding the antigenic polypeptide A means DNAs encoding the polypeptide A. These DNAs are selected from the group of DNAs which are obtained by translating the amino acid sequence for the polypeptide A to triplets in accordance with the genetic code.

As the polypeptide A, those polypeptides which have been described under the item "Antigenic Polypeptides" above may be given. As the DNA encoding the polypeptide A, nucleotides sequences which correspond to the amino acid sequences for those polypeptides may be given.

Similarly, the DNA encoding the polypeptide of SEQ ID NO: 2 means DNAs selected from the group of DNAs which are obtained by translating the amino acids of the polypeptide of SEQ ID NO: 2 to triplets in accordance with the genetic code. This group of DNAs includes the DNA of SEQ ID NO: 4.

Additionally, the DNA encoding the polypeptide of SEQ ID NO: 5 means DNAs selected from the group of DNAs which are obtained by translating the amino acids of the polypeptide of SEQ ID NO: 5 to triplets in accordance with the genetic code. This group of DNAs includes the DNA of SEQ ID NO: 7.

Moreover, the DNA encoding the polypeptide of SEQ ID NO: 6 means DNAs selected from the group of DNAs which are obtained by translating the amino acids of the polypeptide of SEQ ID NO: 6 to triplets in accordance with the genetic code. This group of DNAs includes the DNA of SEQ ID NO: 8.

DNAs encoding the fused proteins comprise codons corresponding to the amino acid sequence of the fused protein. The DNAs include but are not limited to the DNAs of SEQ ID NOs: 17 and 18.

The base sequence of SEQ ID No. 17 is the base sequence of the DNA coding for the fused protein of DHFR and the whole antigen polypeptide of 53 kDa of Chlamydia pneumoniae and the base sequence of SEQ ID No. 18 is the base sequence of the DNA coding for the fused protein of DHFR and (part of) the antigen polypeptide of 53 kDa of Chlamydia pneumoniae.

These DNA's can be manufactured by the method of chemical synthesis or the method of gene recombination.

Among the methods of chemical synthesis is counted the phosphoamidite method which fits the synthesis of a DNA formed in a length of not more than 100 base sequences. This chemical synthesis can be attained by a commercially available DNA synthesizing device.

Among the methods of gene recombination are counted a method f r cloning the DNA from the elementary body of Chlamydia pneumoniae in the manner already described and the PCR method utilizing the already acquired DNA as a template and using a primer manufactured by adopting the base sequence at a position arbitrarily selected in that DNA. The method of gene recombination is capable of manufacturing a long DNA of more than 100 bases.

Now, the method for cloning the DNA coding for the antigen polypeptide from the elementary body of Chlamydia pneumoniae will be described in detail below.

Culture of Chlamydia pneumoniae

A suspension of cells is prepared from cultured HL cells. The supernatant of the culture is removed and the suspension of Chlamydia pneumoniae is then added to the resulting cell sheet. After incubation, Chlamydia pneuminiae-infected HL cells are obtained by centrifugation. As Chlamydia pneumoniae, strain YK41 (Y. Kanamoto et al., Micro biol. Immunol., Vol. 37, p.495-498, 1993) can be used.

Purification of Elementary Body of Chlamydia pneumoniae

The Chlamydia pneuminiae-infected HL cells are disrupted and centrifuged, thereby recovering the supernatant. The obtained supernatant is layered onto a continuous density gradient solution containing Urografin (Schering) is centrifuged.

The yellowish white band was recovered because in the preliminary experiment, it was confirmed to contain the elementary body of Chlamydia pneumoniae with the aid of an electron microscope.

Preparation of Genomic DNA of Chlamydia pneumoniae

The elementary body of Chlamydia pneumoniae is suspended in 10 mM Tris-HCl buffer (pH 8.0) containing 1 mM ethylene diaminetetra acetate (EDTA) (hereinafter referred to as "TE buffer"). To the resulting suspension are added a 1% aqueous solution of sodium dodecyl sulfate (SDS) and an aqueous solution of Proteinase K (1 mg/ml) and the elementary body is lysed while incubating. To the resulting solution is added phenol saturated with 0.1 M Tris-HCl buffer (pH 8.0). The mixture is stirred and centrifuged to recover an aqueous layer. The obtained aqueous layer is treated successively with RNase and phenol/chloroform/isoamyl alcohol, followed by ethanol precipitation. As a result, genomic DNA of Chlamydia pneunomiae is obtained.

Preparation of Genomic DNA Expression Library

The genomic DNA is digested with restriction enzymes AccI, HaeIII and AluI. The digest is treated with phenol/chloroform/isoamyl alcohol and subjected to ethanol precipitation to yield partially digested DNAs. To the partially digested DNAs are added a linker, adenosine 5'-triphosphate (hereinafter abbreviated to "ATP") and T4 ligase, thereby ligating the linker to the partially digested DNAs.

The linker-ligated partially digested DNAs are applied to a Chroma spin 6000 column in which the mobile phase is 10 mM Tris-HCl buffer containing 0.1 M NaCl and 1 mM EDTA. The eluate is collected and fractions containing 1-7 kbp DNA fragments are recovered. To the resulting fractions are added ATP and T4 polynucleotide kinase and a reaction is conducted to phosphorylate the 5' end of the DNA fragments. The reaction solution is treated with phenol/chloroform/isoamyl alcohol and subjected to ethanol precipitation to yield 5'-end-phosphorylated DNA fragments.

To the resulting DNA fragments are added λ gt11 DNA preliminarily digested with restriction enzyme EcoRI, ATP and T4 ligase and a reaction is conducted. The resulting recombinant λ gt11 DNA is packaged with a commercially available packaging kit to prepare a gemonic DNA expression library.

Cloning of DNA Encoding Antigenic Polypeptide

Cultured cells of E. coli strain Y1090r- are infected with the gemonic DNA expression library and incubated in an agar medium. A protein produced in the cells by the expression of the inserted DNA is transferred to a nitrocellulose filter immersed in an aqueous solution of isopropylthio-β-D-galactoside (IPTG). The filter is blocked with a bovine serum albumin and washed. The filter is then reacted with a Chlamydia pneumoniae-specific monoclonal antibody. As the Chlamydia pneumoniae-specific monoclonal antibody, AY6E2E8 and SCP53 can be used. A hybridoma cell line forming AY6E2E8 has been deposited with the National Institute of Bioscience and Human-Technology, the Agency of Industrial Science and Technology (1-3, Higashi 1 chome Tsukubashi Ibaraki-ken 305, Japan) as FERM BP-5154 under the terms of the Budapest Treaty. A hybridoma cell line forming SCP53 is disclosed in J. Clin. Microbil., Vol.132, p.583-588, 1994. After the reaction, the filter is washed and reacted with an anti-mouse IgG antibody labeled with an nzyme such as peroxidase or the like. After the reaction, the filter is washed and reacted with a color-developing substrate solution. As the color-developing substrate solution, a mixture of an aqueous solution of hydrogen peroxide and a solution of 4-chloro-1-naphthol in methanol can be used. After the reaction, the filter is washed and dried in air.

Plaques corresponding to the color-developing spots on th filter are identified and λ phage contained in the plaques is obtained. The above procedure is repeated until all the plaques react with the aforementioned monoclonal antibody. As a result, the DNA encoding an antigenic polypeptide is cloned and λ phage expressing the Chlamydia pneumoniae-specific antigenic polypeptide having reactivity with the Chlamydia pneumoniae-specific monochonal antibody is obtained.

Production of DNA Encoding the Chlamydia pneumoniae-Specific Antigenic Polypeptide

E. coli strain Y1090r- is infected with the obtained λ phage and cultured to yield a large amount of λ phage. DNA molecules are obtained and purified from the λ phage using a commercially available kit. To the obtained DNA molecules are added a primer, Taq polymerase and deoxynucleotides. The steps of heating, cooling and incubating are repeated, thereby amplifying the DNA molecule inserted in λ gt11. λ gt11 forward primer and λ gt11 reverse primer (Takara Shuzo Co. Ltd.) can be used as primers and AmpliTaq DNA polymerase can be used as a Taq polymerase. A general procedure of DNA amplification is known as the PCR method, which is described in detail in J. Sambrook et al., Molecular Cloning, 2nd ed., Cold Spring Harbor Laboratory Press (1989) (hereinafter referred to as "Molecular Cloning").

The amplified DNA is obtained and its base sequence is determined and analyzed. The amplified DNA can be obtained with a commercially available kit such as Wizard PCR Prep kit (Promega). The base sequence can be determined by fluorescence-labeled terminator cycle sequencing using Taq polymerase. This sequencing can be performed with a kit commercially available from Perkin-Elmer Japan. For analysis of the base sequence, a commercially available apparatus such as Model 373A DNA Sequencer (Applied Biosystems) can be used.

Following the determination of the base sequence, the base sequence of the DNA is analyzed using a DNA sequencing software package such as DNASIS (Hitachi Software Engineering) to estimate an editing, junctional and amino acid-translational regions.

If it is found that a full-length gene has not been obtained, DNA molecules upstream and downstream of the available DNA are obtained by genome walking. The genome walking can be performed with a kit commercially available from Takara Shuzo Co., Ltd.

Preparation of DNA Encoding DHFR

DNA encoding DHFR is obtained by digesting the DNA with a restriction enzyme from a plasmid vector containing the DNA or by amplifying the DNA by PCR using a template plasmid DNA or genomic DNA containing the DNA with an appropriate primer.

In the former method, plasmid vector pBBK10MM and recombinant vector pCPN533T of the invention can be used as the plasmid vector containing DNA encoding DHFR. E. coli containing pCPN533T and E. coli containing pBBK10MM have been deposited with the National Institute of Bioscience and Human-Technology, the Agency of Industrial Science and Technology as FERM BP-5222 and FERM BP-2394, respectively. Plasmid pCPN533T can be obtained from the deposited E. coli by a conventional method for obtaining plasmid DNA, which is described in "Molecular Cloning". When plasmid pBBK10MM is used, a DNA fragment having a length of about 4.8 kbp may be excised with restriction enzymes BamHI and XhoI.

In the latter method, pBBK10MM and pCPN533T (see supra) can be used as a plasmid DNA and genomic DNA of Bacillus subtilis can be used as a genomic DNA. Genomic DNA can be obtained by a conventional method for obtaining gemonic DNA, which is described in "Molecular Cloning".

The primer to be used in the latter method can be designed and synthesized in consideration of base sequences at the 5' and 3' ends of DNA encoding DHFR. For example, an oligonucleotide having the 1-20 sequence in the base sequence of SEQ ID NO: 17 and one having a sequence complementary to the 461-480 sequence in the base sequence of SEQ ID NO: 5 can be used. These oligonucleotides can be synthesized chemically with a commercially available DNA synthesizer.

In the antigen polypeptides mentioned above, the polypeptide of SEQ ID NO. 1 containing the whole antigen polypeptide of 53 kDa of Chlamydia pneumoniae is particularly preferred.

Method of Production of Anti-Chlamydia pneumoniae Antibody by Using the Antigenic Polypeptide as Antigen

An anti-Chlamydia pneumoniae antibody can be produced by immunizing a mouse with the antigenic polypeptide of the invention as an antigen, separating a spleen cell from the immunized mouse, fusing the spleen cell with a myeloma cell line to produce hybridomas, selecting a hybridoma recognizing the Chlamydia pneumoniae 53 kDa antigenic polypeptide from the produced hybridomas and culturing the selected hydridoma.

Exemplary myeloma cell lines include P3X63Ag8.653 (ATCC CRL-1580) and P3/NSI/1-Ag4-1 (ATCC TIB-18).

The anti-Chlamydia pneumoniae antibody is produced by a known general procedure for obtaining antibodies by immunization of mouse, except that the antigenic polyp ptide of the invention is used as an antigen.

Method and Reagents for Detection and/or Measurement of Anti-Chlamydia pneumoniae Antibody Using the Antigenic Polypeptide as Antigen, and Agents for Diagnosis of Chlamydia pneumoniae Infections Comprising the Antigenic Polypeptide as Active Ingredient

A method for detection and/or measurement of an anti-Chlamydia pneumoniae antibody comprises, for example, the steps of immobilizing the antigenic polypeptide on a support, applying a sample, washing, adding a labeled secondary antibody, washing and detecting and/or measuring the label either directly or indirectly.

Examples of the support include latex particles, cellulose threads, plastic assay plates and particles and the like.

The antigenic polypeptide may be immobilized on the support through covalent bonding or physical adsorption.

Examples of the sample include human sera and the like. It is preferred to block the surface of the support with bovine serum albumin or the like before the addition of a sample so as to insure that other antibodies in the sample will not bind to the support unspecifically.

The support is washed with a surfactant-containing phosphate buffer or the like.

An example of the labeled secondary antibody is a labeled anti-human monoclonal antibody. Useful labels include various kinds of enzymes such as alkaline phosphatase, luciferase, peroxidase, β-galactosidase and the like, various fluor scent compounds such as fluorescein and the like. A chemical compound such as biotin, avidin, streptoavidin, digoxigenin or the like may be inserted between the antibody and the label.

When the label is an enzyme, it may be detected and/or measured by adding a substrate and detecting and/or measuring the light emission or color development which occurs due to the catalytic action of the enzyme or by measuring the change in light absorbance. When the label is a fulorescent compound, it may be detected and/or measured by irradiating the reaction system with UV light and detecting and/or measuring the emitted fluorescence. A sensitizer may be used if necessary.

Reagents for detection and/or measurement of the anti-Chlamydia pneumoniae antibody using the antigenic polypeptide of interest as an antigen include the antigenic polypeptides which are immobilized on a support and those with which the necessary amounts of the secondary antibody and the substrate are enclosed.

The aforementioned reagents can be used as agents for diagnosis of Chlamydia pneumoniae infections.

Probes and Primers for Detection and/or Measurement of Chlamydia pneumoniae Gene

DNA encoding the Chlamydia pneumoniae 53 kDa antigenic polypeptide has the base sequence of SEQ ID NO: 3.

The probes and primers of the invention comprise DNA containing any one of

(a) a DNA containing a sequence of at least 10 consecutive bases in the DNA of SEQ ID NO: 3,
(b) a DNA complementary to DNA (a), or
(c) a DNA having at least 90% homology to DNA (a) or (b).

The length of the base sequence of the probes and primers is preferably 10-50 bp, more preferably 15-20 bp.

Specific examples of the probes and primers of the invention include a DNA comprising the base sequence of SEQ ID NO: 19 and a DNA comprising the base sequence of SEQ ID NO: 20.

The probes and primers of the invention can be synthesized easily with a commercially available DNA synthesizer. DNA synthesizers are commercially available from Applied Biosystems and the like. Alternatively, the probes and primers of the invention can be prepared by chemically synthesizing a short DNA fragment and synthesizing a long DNA fragment by PCR using the short DNA as a primer.

The probes and primers of the invention include those prepared by labeling such DNAs.

Exemplary labels include chemical compounds such as biotin, avidin, streptoavidin, digoxigenin and the like; enzymes such as alkaline phosphatase, luciferase, peroxidase, β-galactosidase and the like; and fluorescent compounds such as fluorescein and the like. Biotin may be bound to the probes by, for example, adding biotinated deoxyuridine 5'-triphosphate to the probes in the presence of a terminal transferase. A kit containing a terminal transferase and biotinated deoxyuridine 5'-triphosphate can be purchased from Boehringer Mannheim. In the case where a label other than biotin is to be bound, a commercially available kit can also be used. Such a kit can be purchased from Takara Shuzo Co., Ltd and TOYOBO CO., LTD. Alternatively, the label may be bound by a method described in "Molecular Cloning".

If desired, radioactive isotopes can be used as labels. In this case, (γ-^{32}P)dATP is added to the probes and primers in the presence of T4 polynucleotid kinase. A general procedure of labeling with a radioactive isotope is described in "Molecular Cloning". T4 polynucleotide kinase can be purchased from TOYOBO CO., LTD. and (γ-^{32}P)dATP from Amersham.

RNAs corresponding to the base sequences of the probes and primers of the invention, that is, nucleic acids in which thymine is replaced with uracil in the base moiety and in which deoxyriboses are replaced with riboses in the sugar chain, can be used as the probes and primers of the invention instead of the aforementioned probes and primer

comprising DNAs as structural units. These probes and primers comprising RNAs as structural units can be used in the method and reagents for detection and/or measurement of the invention.

Method for Detection and/or Measurement of Chlamydia pneumoniae Gene

Chlamydia pneumoniae gene is detected and/or measured by, for example, separating DNA in a sample on the basis of the difference in molecular weight by elecrophoresis, transferring the obtained DNA to a nitrocellulose filter, nylon membrane filter or the like for its identification, adding the labeled probe of the invention, and detecting and/or measuring the label. This method is called the Southern blotting technique and its general procedure is described in "Molecular Cloning".

Chlamydia pneumoniae gene is detected and/or measured with the primer of the invention by, for example, the PCR method which was described above. The method for detecting and/or measuring Chlamydia pneumoniae gene by PCR using the primer of the invention comprises the following steps.

(i) A buffer containing the primer of the invention, DNA polymerase, dATP, dCTP, dGTP and dTTP is added to a sample containing DNA and the mixture is heated.
(ii) The reaction solution is cooled, held at a constant temperature and heated.
(iii) Step (ii) is repeated.
(iv) The DNA contained in the reaction solution is detected and/or measured.

The DNA-containing sample to be used in step (i) may be nucleic acids as extracted from tunica mucosa pharyngsis of a patient.

The DNA polymerase to be used in step (i) may be a Taq polymerase, which can be purchased from TOYOBO CO., LTD.

In step (i), the mixture is heated by, for example, leaving it to stand at 90-100°C for 0.5-10 minutes.

In step (ii), the reaction solution is cooled by, for example, leaving it to stand at 45-65°C for 0.5-5 minutes, held at a constant temperature by, for example, at 70-80°C for 1-10 minutes, heated by, for example, leaving it to stand at 90-100°C for 0.5-5 minutes.

The heating in step (i), and cooling, holding at a constant temperature and heating in step (ii) can be carried out by using a DNA thermal cycler® (Perkin-Elmer Cetus).

Step (iii) may be repeated any number of times, preferably about 30 times.

The DNA contained in the reaction solution is detected and/or measured in step (iv) by, for example, electrophoresing the reaction solution with an agarose gel containing ethidium bromide, and thereby separating the DNA in the reaction solution on the basis of the difference in molecular weight and irradiating the agarose gel with UV light. If the primer of the invention is a labeled one, DNA is detected and/or measured with the aid of the label.

In another embodiment of the invention, after steps (i)-(iii), the primer of the invention may be replaced with one having another base sequence and steps (i)-(iii) are repeated, followed by step (iv).

Reagents for Detection and/or Measurement of Chlamydia pneumoniae Gene

An exemplary reagent for detection and/or measurement of Chlamydia pneumoniae gene according to the invention is an aqueous solution of the probe or primer of the invention which is packed frozen in a plastic container.

BEST MODE FOR CARRYING OUT THE INVENTION

Now, this invention will be described in detail below with reference to examples. It is to be distinctly understood that the invention is not limited in any sense to these examples.

Now, the component steps of the process from the culture of host cells of Chlamydia pneumoniae through the determination of gene DNA sequence/amino acid sequence of the antigenic polypeptide of Chlamydia pneumoniae will be described below in the order of their occurrence.

Example 1: Preparation of DNA coding for 53K antigenic polypeptide specific to Chlamydia pneumoniae

(A) Culture of host cells (HL cells)

The HL cells cultured in advance confluently on the bottom surface of a plastic culture flask (75 cm^2) were washed with 5 ml of a magnesium-free (-) solution of a phosphate buffer physiological saline solution (hereinafter referred to as "PBS"), coated throughout on the entir surface thereof with 5 ml of a PBS containing 0.1% (w/v) trypsin, deprived of the excess solution, kept warmed at 37 °C for 10 minutes, and made to add 5 ml of a Dulbecco MEM culture medium

containing 10% (v/v) bovine fetal serum. The HL cells adhering to the flask interior were removed by pipetting to obtain a cell suspension.

The culture in a plastic culture flask (75 cm^2) was implemented by charging the culture flask with 1 ml of the cell suspension mentioned above and 5 to 20 ml of the Dulbecco MEM culture medium containing 10% (v/v) bovine fetal serum and the culture in a 6-well plastic culture vessel was effected by placing in each of the six wells 4 ml of a mixed solution consisting of 8 ml of the cell suspension mentioned above and 292 ml of the Dulbecco MEM culture medium containing 10% bovine fetal serum and performing culture under an ambience containing 5% (v/v) carbon dioxide gas.

(B) Culture of Chlamydia pneumoniae YK41

From the culture solution of the HL cells propagated in a 6-well plastic culture vessel (on the bottom surface thereof), the supernatant was removed with a pipet. The residual cell sheet in the culture vessel, after adding 2 ml per well of the suspension of the YK41 strain of Chlamydia pneumoniae (Kanamoto et al., Microbiol. Immunol., Vol. 37, p.495-498, 1993) [the supernatant obtained by diluting a preserved solution of Chlamydia pneumoniae YR41 to 12 to 24 times the original volume with an aqueous solution containing 75 g of sucrose, 0.52 g of monopotassium phosphate, 1.22 g of dipotassium phosphate, and 0.72 g of glutamic acid liter (hereinafter referred to as "SPG"), treating the diluted solution with a supersonic wave for one minute, and subjecting the resultant diluted solution to centrifugal separation at 2,000 rpm for three minutes], was subjected to centrifugal adsorption at 2,000 rpm for one hour. After the centrifugal adsorption, the Chlamydia pneumoniae suspension was removed from the resultant cell sheet. The residual cell sheet, after adding 4 ml per well of a Dulbecco MEM culture medium containing 1 μg of cyclo-heximide per ml and 10% (v/v) of bovine fetal serum, was cultured at 36 °C for three days under an ambience containing 5% (v/v) carbon dioxide gas. After this culture, the cells adhering to the culture vessel were separated with a sterilized silicone blade and recovered. Th cells were centrifuged at 8,000 rpm for 30 minutes. The sediment obtained consequently was resuspended in SPG and the resultant suspension was put to storage at -70 °C.

(C) Purification of elementary body of Chlamydia pneumoniae YK41

The frozen suspension of HL cells infected with the Chlamydia pneumoniae YK41 preserved at -70 °C was melted and homogenized by the use of a homogenizer. The homogenate was centrifugally separated at 2,500 rpm for 10 minutes and the supernatant consequently formed was recovered. The sediment was again suspended in SPG and treated in the same manner as described above to recover a new supernatant. This procedure was repeated twice more. The succ ssive supernatants were joined into one volume.

Separately, in a centrifuging tube, a 0.03M tris-hydrochloride buffer (pH 7.4) containing 50% (w/v) sucrose was placed, then a mixed solution of 3 parts by volume of urografin 76% (produced by Schering Corporation) with 7 parts by volume of 0.03M tris hydrochloride buffer (pH 7.4) was superposed, and subsequently the supernatant recovered as described above was attentively superposed on the layer of the mixed solution. The superposed layers in the centrifuging tube were centrifuged at 8,000 rpm for one hour. The layer of the 0.03M tris hydrochloride buffer (pH 7.4) containing 50% (w/v) sucrose and the sediment were recovered from the tube. The recovered solution and SPG added thereto in an equal volume were subjected to centrifugation at 10,000 rpm for 30 minutes. From the resultant separated phases, th supernatant was discarded and the sediment was suspended in SPG. In the centrifuging tubes, continuous density-gradient solutions consisting 35% to 50% of Urografin 76% (produced by Schering Corporation) in 0.03M tris hydrochloride buffer (pH 7.4) (ratios by volume of the former component to the total volume of solution) were placed and the suspension mentioned above was superposed thereon. The superposed layers in the tubes were centrifuged at 8,000 rpm for one hour. When a small amount of the yellowish white band was sampled and observed under an electron microscope, it was found to contain the elementary body of Chlamydia pneumoniae. So, this band was recovered and diluted with SPG to twice the original volume, and centrifuged at 10,000 rpm for 30 minutes. The sediment obtained in consequence of the centrifugation was suspended in SPG, assayed for protein concentration (with the aid of a protein analysis kit produced by Biorad Corp, with bovine serum albumin as a standard), and put to storage at -70 °C.

(D) Preparation of genome DNA of Chlamydia pneumoniae YK-41 strain

Three hundred (300) μl of a suspension of the elementary body of the purified Chlamydia pneumoniae YK-41 strain mentioned above (protein concentration: 1.37 mg/ml) was centrifuged at 4 °C at 12,000 rpm for five minutes. The resultant sediment was susp nded in 500 μl of 10 mM tris buffer (pH 8.0) containing 1 mM EDTA (her inafter referred to as "TE buffer"). The same centrifugation was repeated and the resultant sediment was suspended in 300 μl of TE buffer. The produced suspension and 30 μl of an aqueous 2% SDS solution and 30 μl of an aqueous solution of 1 mg/ml proteinase K added thereto were incubated at 56 °C for 30 minutes to effect solution of the elementary body. The incubated solution and 350 μl of phenol-saturated 0.1M tris hydrochloride buffer (pH 8.0) added thereto were thoroughly stirred with a vortex mixer. The resultant mixture was centrifuged at 4 °C at 12,000 rpm for five minutes. From the separated

layers, the aqueous layer was recovered (for extraction of DNA). This procedure of extraction was repeated once more. The aqueous layer and 2 µl of a 10 mg/ml RNase solution added thereto were incubated at 37 °C for two hours to effect decomposition of RNA. The incubated solution and 300 µl of a mixed solution consisting of a phenol-saturated 0.1M tris-hydrochloride buffer (pH 8.0), chloroform, and isoamyl alcohol at a volumetric ratio of 25 : 24 : 1 (hereinafter referred to as "PCI") were thoroughly stirred with a vortex mixer. The resultant mixture was centrifuged at 4 °C at 12,000 rpm for five minutes. From the separated layers, the aqueous layer was recovered. This procedure was repeated until a fifth time.

One part by volume of the resultant solution and 1/10 part by volume of an aqueous 10M ammonium acetate solution and two parts by volume of ethanol added thereto were left standing for five minutes to effect precipitation of DNA. The resultant mixed solution was centrifuged at 4 °C at 12,000 rpm for five minutes. The sediment plus 600 µl of an aqueous 70% ethanol solution was thoroughly stirred and centrifuged at 4 °C at 12,000 rpm for five minutes to effect purification. This procedure was repeated twice more. The contents of the centrifuging tubes were left standing for 15 minutes with the lids of the tubes kept open to dry the sediment. The dry sediment was dissolved with 200 µl of TE and the resultant solution was put to storage at -20 °C.

(E) Preparation of genome DNA expression library

One hundred (100) µl of a genome DNA solution and 10 µl of a restriction endonuclease grade M-buffer and 10 µl of a restriction endonuclease mixed solution (obtained by mixing 0.4 µl each of AccI, Hae III, and 1/50 dilution AluI with 20 µl of TE) added thereto were left reacting at 37 °C for 20 minutes. The reaction time of 20 minutes mentioned above was a duration necessary for DNA to be decomposed into partially digested DNA fractions of sizes ranging from 1 kbp through 7 kbp. It was empirically found in advance by using a small amount of genome DNA. The resultant reaction solution and 100 µl of PCI added thereto were thoroughly stirred with a vortex mixer and the produced mixture was centrifuged at 4 °C at 12,000 rpm for five minutes. The aqueous phase was recovered from the separated layers consequently obtained. The recovered aqueous layer and 10 µl of an aqueous 3M sodium acetate solution and 220 µl of ethanol added thereto were left standing at -80 °C for 15 minutes to effect precipitation of partially digested DNA. The produced mixed solution was centrifuged at 4 °C at 12,000 rpm for five minutes. From the separated layers, the supernatant was discarded. The sediment was mixed with 600 µl of an aqueous 70% ethanol solution and the produced mixture was again centrifuged at 12,000 rpm for five minutes. The supernatant was discarded and the sediment was dried under a reduced pressure.

The partially digested DNA consequently obtained was dissolved in 20 µl of purified water. The amount 19 µl of the DNA solution and 14 µl of a linker (20 pmole/µl) represented by the following base sequence, 4.5 µl of 10 mM ATP, 4.5 µl of a 0.2M tris-hydrochloride buffer (pH 7.6; hereinafter referred to as "tenfold concentration ligation grade buffer") containing 50 mM $MgCl_2$, 50 mM dithiothreitol, and 500 µg/ml bovine serum albumin, 2 µl of purified water, and 1 µl of T4 ligase added thereto were left reacting at 16 °C for four hours to effect addition of the linker.

5'-AATTCGAACCCCTTCG-3'

3'-GCTTGGGGAAGCp-5'

The partially digested DNA adding the linker as described above was treated with a column (Chroma Spin 6000) using a 10 mM tris-hydrochloride buffer containing 0.1M NaCl and 1 mM EDTA as a migration phase. From the eluate, fractions each of two drops were separated. Each fraction was partly analyzed by 0.8% agarose gel electrophoresis to recover a fraction containing DNA segments of sizes from 1 kbp through 7 kbp. The amount 144 µl of the produced fraction and 13 µl of purified water, 20 µl of 10 mM ATP, 20 µl of a 0.5M tris-hydrochloride buffer (pH 7.6 maximum; hereinafter referred to as "tenfold concentration phosphorization grade buffer") containing 0.1M $MgCl_2$, 50 mM dithiothreitol, 1 mM spermidine hydrochloride, and 1 mM EDTA, and 3 µl of T4 polynucleotide kinase added thereto were left reacting at 37 °C for 30 minutes to effect phosphorization of the 5' terminal of the DNA fragment. The resultant reaction solution and 200 µl of PCI added thereto were thoroughly mixed by shaking. The produced mixture was centrifuged at 4 °C at 12,000 rpm for five minutes. From the separated layers, the aqueous layer was recovered. The aqueous phase was made to precipitate nucleotide by addition of 1 µl of an aqueous 20 mg/ml glycogen solution, 20 µl of an aqueous 3M sodium acetate solution, and 400 µl of ethanol. The produced solution was centrifuged at 4 °C at 12,000 rpm for 10 minutes. The supernatant was discarded. The sediment was mixed with 200 µl of 70% ethanol and again centrifuged. From the separated layers, the supernatant was discarded. The sediment was air dried and then dissolved in, 1 µl of purified water.

The amount 0.6 µl of the resultant aqueous solution and 1 µl of λ gtII DNA (1 µg/µl, produced by Stratagene Corp.) cleaved in advance with a restriction endonuclease EcoRI, 0.5 µl of a tenfold concentration ligation grade buffer, 0.5 µl of 10 mM ATP, 0.4 µl of T4 ligase, and 2 µl of purified water added thereto were left reacting overnight at 4 °C. Then, the recombinant λ gtII DNA consequently obtained was packaged by the use of a packaging kit (produced by Stratagene Corp. and marketed under trademark designation of Gigapack II Gold").

(F) Production of Chlamydia pneumoniae-specific monoclonal antibody

Cultivation and transfer of the myeloma cell strain

The myeloma cell strain used for the production of the monoclonal antibody was P3/NSI/1-Ag 4-1 (ATCC TIB-18). It was incubated and subjected to successive transfer culture in the RPMI 1640 culture medium containing 10% (v/v) bovine fetal serum. Two weeks prior to the cell fusion, the strain was incubated for one week in the RPMI 1640 culture medium containing 0.13 mM of 8-azaguanine, 0.5 μg/ml of a mycoplasma expellant (produced by Dainippon Pharmaceutical Co., Ltd. and marketed under product code of "MC-210"), and 10% (v/v) bovine fetal serum and then it was incubated in a standard culture medium for one week.

Immunization of mouse

Two hundred (200) μl of the suspension of the aforementioned elementary body having a protein concentration of 270 μg/ml was centrifuged at 12000 rpm for 10 minutes. The precipitate and 200 μl of PBS added thereto were together suspended. The suspension was emulsified by the addition of 100 μl of Freund's adjuvant. A portion, 150 μl in volume, of the emulsion was hypodermally injected into the back of a mouse (0'th day of experiment). On the 14th, 34th, and 49th day, the suspension of the purified elementary body having a protein concentration of 270 μg/ml was intra-abdominally injected in a fixed dose of 100 μl into the mouse. Further, 50 μl of the suspension of the purified elementary body having a protein concentration of 800 μg/ml was intra-abdominally injected into the mouse on the 69th day and 100 μl of the same suspension was similarly injected into the mouse on the 92nd day. On the 95th day, the mouse was sacrificed to extract the spleen, which was put to use in the cell fusion.

Cell fusion

In a round bottom glass tube, 10^8 spleen cells obtained from the spleen of the immunized mouse and 10^7 myeloma cells were thoroughly mixed and centrifuged at 1400 rpm for five minutes. The supernatant was removed and the remaining cells were further mixed thoroughly. The cells and 0.4 ml of the RPMI 1640 culture medium containing 30% (w/v) polyethylene glycol and kept in advance at 37°C were together left standing at rest for 30 seconds. The resultant mixture was centrifuged at 700 rpm for six minutes. The glass tube containing this mixture and 10 ml of the RPMI 1640 culture medium added anew thereto was slowly rotated to ensure thorough dispersion of polyethylene glycol and centrifuged at 1400 rpm for five minutes. The supernatant was completely removed. The precipitate and 5 ml of the HAT culture medium added thereto were together left standing at rest for five minutes. The resultant mixture and 10 - 20 ml of the HAT culture medium added thereto were together left standing at rest for 30 minutes and then diluted by the addition of the HAT culture medium until the myeloma cell concentration reached 3.3×10^5/ml to suspend the cells. The suspension was dispensed two drops each to the wells of a 96-well plastic incubation vessel by the use of a Pasteur's pipet. The suspension was incubated in the atmosphere of 5% (v/v) carbon dioxide gas at 36°C. After one day, 7 days, and 14 days following the start of the incubation, the HAT culture medium was added one to two drops each to the wells.

Screening of antibody-producing cells

The purified elementary body of the Chlamydia pneumoniae YK 41 strain was solubilized with 1% (w/v) SDS, dialyzed against a 0.05M sodium bicarbonate buffer solution (pH 9.6) containing 0.02% of sodium azide, diluted until the protein concentration reached a level in the range of 1 - 10 μg/ml, dispensed 50 μl each to the wells of a 96-well EIA grade plate made of vinyl chloride, and left standing at rest overnight at 4°C to induce adsorption of the antigen. The supernatant was removed. 150 μl of the PBS containing 0.02% (w/v) Tween 20 was added to the wells and the plate was left standing at rest for three minutes. The wells were deprived of the PBS and cleaned. After the wells were given a cleaning treatment once more, 100 μl of the PBS containing 1% (v/v) bovine serum albumin was added to the wells and left standing at rest overnight at 4°C to effect blocking. The wells were deprived of the PBS containing the bovine serum albumin, cleaned twice in the same manner as above with the PBS containing 0.02% (w/v) Tween 20 and, after adding 50 μl of the culture supernatant of the fused cells, left at rest at room temperature for two hours. The wells were cleaned three times in the same manner as above with the PBS containing 0.02% (w/v) Tween 20 and, after adding 50 μl of the goat anti-mouse IgG antibody (25 ng/ml) labeled with peroxidase, left standing at rest at room temperature for two hours. The wells were cleaned three times in the same manner as above with the PBS containing 0.02% (w/v) Tween 20 and, after adding 50 μl of the ABTS solution (produced by KPL Corp.), left standing at rest at room temperature for 15 minutes - one hour to induce a coloring reaction. The contents of the wells were tested for absorbance at 405 nm by the use of a 96-well EIA plate grade photometer.

As a result, positive wells were detected and the supernatants of culture broth in these wells were found to contain an antibody capable of reacting the elementary body. The cells in these wells were recovered severally with the Pas-

teur's pipet, transferred to a 24-well plastic incubation vessel and, after adding 1 - 2 ml of the HAT culture medium, incubated in the same manner as above.

Cloning by limiting dilution method

The fused cells propagated in the 24-well plastic incubation vessel were tested for cell concentration and diluted with the HT culture medium to adjust the number of cells to 20/ml. Separately, the thymocytes of 4- to 6-week old mice suspended in the HT culture medium were dispensed to a 96-well plastic culture vessel at a rate of 2 x 10^5/well and, after adding the aforementioned fused cells (cell concentration 20/ml) at a rate of 50 µl/well, incubated in an atmosphere of 5% (v/v) carbon dioxide gas at 36°C. After 1 day, 7 days, and 14 days following the start of the incubation, the HT culture medium was added to the culture vessel at a rate of 1 to two drops/well. From the wells observed to have propagated cells, the supernatant of the culture broth was recovered in a fixed volume of 50 µl per well and then analyzed in the same manner as above to confirm the production of an antibody.

From the wells in which only one cell colony was present, cells producing an antibody able to react with the elementary body and showing quick propagation were recovered and allowed to continue propagation in a 24-well plastic culture vessel. The same cloning procedure was repeated until a hybridoma AY6E2E8 was ultimately obtained.

Production of monoclonal antibody

The hybridoma AY6E2E8 was cultured in a 75 cm^2 plastic cell culture flask holding therein 20 ml of the RPMI 1640 culture medium containing 10% (v/v) bovine fetal serum. From the culture broth formed in the flask, a sample, 16 - 18 ml in volume, was extracted at intervals of three to four days. The residual culture broth was meanwhile replenished to a total volume of 20 ml with a fresh supply of the RPMI 1640 culture medium containing 10% (v/v) bovine fetal serum. Thus, the subculture of the hybridoma was continued. The samples extracted from the culture broth were centrifuged at 1200 rpm for five minutes to recover the supernatant (the culture supernatant containing the monoclonal antibody).

To a Balb/c mouse which had received intra-abdominal injection of 0.5 ml of pristane two weeks in advance of the experiment, the hybridoma strain suspended in the PBS at a concentration of 1 - 5 x 10^6/ml was intra-abdominally injected in a volume of 1 ml. After three weeks thence, the ascites was recovered from the Balb/c mouse and centrifuged at 1200 rpm for five minutes to recover the supernatant (ascites containing the monoclonal antibody).

Identification of subclass of monoclonal antibody

The subclass of the monoclonal antibody was identified with the ISOTYPE Ab-STAT (produced by Sang Stat Medical Corp.). As a result, the subclass of the monoclonal antibody produced by the hybridoma AY6E2E8 was identified to be IgG2b.

Purification of monoclonal antibody

The monoclonal antibody produced by the hybridoma AY6E2E8 was purified as follows. A mixture of 1 part by volume of the monoclonal antibody-containing ascites obtained by injecting the hybridoma AY6E2E8 intra-abdominally to the mouse with 3 parts by volume of PBS was centrifuged at 3000 rpm for ten minutes. The resultant supernatant was passed through a filter, 0.22 µm in pore size. The filtrate was purified by the HPLC using Chromatop Superprotein A Column (4.6 mm Diam. x 100 mm, produced by NGK Insulators Ltd. This column was equilibrated with the PBS in advance of the treatment.

A sample, 1 ml in volume, of the filtrate emanating from the 0.22 µm filter was injected into the column. The column was washed by passing the PBS first at a flow rate of 1 ml/min for three minutes and then at a flow rate of 5 ml/min for four minutes. The monoclonal antibody adsorbed on the column was eluted by passing a solution of 8.77 g of NaCl, 16.7 g of citric acid (monohydrate), and 14.72 g of Na2HPO4 • 12H2O in 1 liter of purified water through the interior of the column at a flow rate of 2 ml/min for five minutes. The fractions of the desorbed monoclonal antibody were gathered and diluted with a TTBS solution.

The elementary body of Chlamydia pnuemoniae was dissolved to obtain the peptide contained in the elementary body. The peptide and the monoclonal antibody mentioned above were subjected to the Western blotting to determine the specificity of the acquired monoclonal antibody.

As a result, the acquired monoclonal antibody was found to be capable of recognizing the Chlamydia pneumonia 53 kDa antigen polypeptide.

A hybridoma 70 was acquired in the same manner as the hybridoma AY6E2E8. When the monoclonal antibody producing the hybridoma 70 was tested for specificity by following the procedure described above, it was found that this monoclonal antibody was capable of recognizing the Chlamydia pneumoniae 73 kDa antigen polypeptide.

When the monoclonal antibody produced by the hybridoma 70 was examined in the same manner as above by way

of identification of subclass, the subclass of this antibody was found to be IgG.

(G) Cloning of DNA coding for antigenic polypeptide

One platinum loop full of the Y1090r-strain of Escherichia coli was inoculated to an LB (containing 5 g of NaCl, 10 g of polypeptone, and 5 g of yeast extract per liter of water) culture medium containing 0.2% maltose and 50 μg/ml of ampicillin and shaken cultured at 37 °C overnight. The resultant culture solution was centrifuged at 2,000 rpm for 10 minutes. The sediment (Escherichia coli) was mixed with 9 ml of an aqueous 10 mM MgSO 4 solution. The amount 0.35 ml of the Escherichia coli suspension and 0.1 to 10 μl of the λ gtll (DNA library) suspension added thereto were incubated at 37°C for 20 minutes to infect the Escherichia coli with λ gtll. The λ gtll-infected Escherichia coli mentioned above was added to 2.5 ml of a liquid LB agar culture medium kept warmed in advance at 47 °C and the resultant mixture was scattered on an LB agar culture medium. After the upper-layer culture medium was solidified, the entire culture medium was cultured at 42 °C for three to four hours. At the time that a plaque was observed, a nitrocellulose filter (containing perforations 82 mm in diameter) immersed in advance in an aqueous 10 mM IPTG solution was mounted in the upper-layer agar culture medium. Then, the whole culture medium was cultured at 37 °C for 12 hours. With a syringe having the tip of the nozzle thereof smeared with black ink, the filter was pierced at three asymmetrical points selected as marks on the filter. Then, the filter now bearing the marks of the black ink was extracted from the agar culture medium and washed three times with a 20 mM tris-hydrochloride buffer (pH 7.5) containing 150 mM NaCl and 0.1% Tween 20 (hereinafter referred to as "TTBS buffer"). The residual agar culture medium was put to storage in a refrigerator.

The filter was immersed in a 0.1% bovine serum albumin-containing solution of a 20 mM tris-hydrochloride buffer (pH 7.5) containing 150 mM NaCl (hereinafter referred to as "TBS buffer") and shaken at 37 °C for one hour to effect a blocking reaction thereon. Then, the filter was washed twice with the TTBS buffer, immersed in the 10 μg/ml TTBS solution of a monoclonal antibody specific to Chlamydia pneumoniae, and shaken at 37 °C for one hour. The filter was washed three times with the TTBS buffer and then shaken in a peroxidase-labelled anti-mouse IgG antibody solution (TTBS buffer, 50 ng/ml) at 37 °C for one hour. The filter was washed three times with the TTBS buffer and three times with the TBS buffer, then immersed in a color ground substance solution (prepared by adding 60 μl of an aqueous 30% hydrogen peroxide solution and 20 ml of a methanolic 0.3% 4-chloro-1-naphthol solution to 100 ml of the TBS buffer), and left standing therein at room temperature for about 30 minutes. At the time that the filter was thoroughly colored, this filter was extracted from the solution, washed with purified water, and air-dried.

The plaques formed on the agar culture medium at the positions corresponding to the colored spots on the filter were searched out and identified. The relevant portions of the agar were pierced with a Pasteur pipet to recover the plaques. Each recovered plaque was placed in a 50 mM tris-hydrochloride buffer (pH 7.5) containing 0.1 M NaCl, 8 mM magnesium sulfate, and 0.01% gelatin (hereinafter referred to as "SM buffer") and one drop of chloroform, and left standing therein at 4 °C overnight to effect extraction of the λ phage from the plaque. The procedure just described was repeated until the plaque wholly reacted with the monoclonal antibody mentioned above to obtain a clone of the DNA coding for the antigen polypeptide.

As a result, the λ phage which expressed a Chlamydia pneumoniae-specific antigen polypeptide reactive with a Chlamydia pneumoniae-specific monoclonal antibody was obtained and designated as 53-3S λ phage.

(H) Culture of 53-3S λ phage and purification of DNA

Plaques were formed by following the procedure described in (F) above. One of the plaques was recovered, placed in 100 μl of the SM buffer, and left standing therein at 4 °C overnight to effect extraction of the λ phage. In the LB culture medium in which 250 μl of the Y1090r- strain of Escherichia coli was cultured overnight, 5 to 10 μl of the λ phage solution was placed and left standing therein at 37 °C for 20 minutes to effect infection of the Escherichia coli with the λ phage. The infected Escherichia coli was inoculated to 50 ml of the LB culture medium containing 10 mM magnesium sulfate and kept warm in advance at 37 °C and shaken cultured therein at 37 °C for five to seven hours until the bacteriolysis of the Escherichia coli by the λ phage occurred. The resultant culture solution, after adding 250 μl of chloroform, was centrifuged at 3,000 rpm for 10 minutes to effect removal of the residual cells of Escherichia coli and obtain a suspension of the λ phage. The λ phage DNA was purified by the use of a special device (produced by Promega Corp. and marketed under trademark designation of "Wizard λ Preps Kit").

(I) Amplification of DNA coding for Chlamydia pneumoniae antigenic polypeptide

A 600 μl grade microtube was charged with 61.5 μl of purified water, 10 μl of a tenfold concentration of reaction buffer (a tris-hydrochloride buffer, pH 8.3, containing 500 mM KCl, 15 mM $MgCl_2$, and 0.01% gelatin), 1 μl of 20 mM dNTP, 0.1 μl of 53-3S λ phage DNA solution, 1 μl of 20 nM λ gtll forward primer (produced by Takara Shuzo Co., Ltd.), 1 μl of 20 nM λ gtll reverse primer (produced by Takara Shuzo Co., Ltd.), and 0.5 μl of AmpliTaq DNA Polymerase, with

two or three drops of mineral oil placed to form a top layer. The contents of the microtube were subjected to 30 circles of incubation, each consisting of 30 seconds' standing at 94 °C, 30 seconds' standing at 55 °C, and two minutes' standing at 73 °C to effect amplification of the DNA. After the reaction, the reaction solution was subjected to 1.2% low-melting temperature agarose gel electrophoresis to excise the amplified DNA. This amplified DNA was purified by the use of "Wizard PCR Prep Kit" (produced by Promega Corp.).

(J) Analysis for DNA base sequence

The analysis of the DNA for base sequence was effected by subjecting a sample to a sequence reaction in accordance with the fluorescence-labelled terminator cycle sequence method using a Taq DNA polymerase with a PCR-amplified DNA as a template and analyzing the reaction product by a DNA sequencer (produced by Applied Biosystems Corp. and marketed under product code of "Model 373A"). The DNA base sequence consequently obtained was examined by the gene sequence analysis soft (produced by Hitachi Software Engineering Co., Ltd. and marketed under trademark designation of "DNASIS") to estimate agglutination, ligation, and amino acid translation region. Consequently, the sequence was identified as SEQ ID No: 9.

The results of the analysis of the sequence of SEQ ID No: 9 show that about 60% of the amino acid sequence of the 53KDa antigenic polypeptide from the N terminal thereof toward the C terminal was elucidated.

The DNA which codes for the Chlamydia pneumoniae antigen polypeptide is specific to Chlamydia pneumoniae and it has been cloned by utilizing a monoclonal antibody recognizing the 53 Kda antigen polypeptide. Thus, this DNA apparently encodes the 53 kDa antigen polypeptide.

The search for homology of both the base sequence and the amino acid sequence of SEQ ID No: 9 was carried out in accordance with the GenBank data base confirmed absence of a known series exhibiting high homology.

Example 2: Preparation of recombinant vector containing DNA coding for polypeptide containing part of antigenic polypeptide of Chlamydia pneumoniae, and preparation of transformant carrying the vector.

Though the acquired DNA evidently coded for the 53 KDa antigen polypeptide as mentioned above, it was expressed as shown below to determine whether or not it would react with the antibody mentioned above by way of precaution.

A plasmid pBBK10MM was severed with restriction enzymes of BamHI and XhoI and subjected to 1.2% low melting temperature solution agarose gel electrophoresis to excise about 4.6 Kbp of DNA fragment. This fragment was purified. The synthetic DNA's of SEQ ID No: 11 and SEQ ID No: 12 were added each in an amount of 1 ng to 100 ng of the DNA fragment and they were ligated by the use of a DNA ligation kit (produced by Takara Shuzo Co., Ltd.) The resultant reaction product was placed in an Escherichia coli HB101 strain-competent cell (produced by Takara Shuzo Co., Ltd.) to prepare a transformant and acquire a plasmid, which was designated as pADA431. This plasmid was severed with a restriction enzyme MunI and then subjected to an alkali phosphatase reaction to effect removal of the 5' phosphoric acid base.

Separately, the 53-3S λ phage DNA was severed with a restriction enzyme EcoRI. One hundred (100) ng of the pADA431 plasmid DNA severed with the restriction enzyme MunI mentioned above was added to 50 ng of the DNA fragment and they were ligated in the same manner as described above to prepare a transformant and acquire a plasmid incorporating therein the restriction enzyme EcoRI fragment of 53-3S λ phage DNA, which was designated as pCPN533 α. This plasmid was a DNA of a length of about 5.7 kbp possessing a base sequence of SEQ ID No: 10 and was capable of expressing the polypeptide containing part of 53K antigenic polypeptide with a host Escherichia coli. The base sequence of the DNA coding for the polypeptide containing part of the 53K antigenic polypeptide was shown by SEQ ID No: 4. The amino acid sequence deduced from this base sequence was shown by SEQ ID No: 2. An Escherichia coli carrying the plasmid pCPN533a was subjected to culture, electrophoresis, transfer to a nitrocellulose membrane, and detection with a monoclonal antibody in the same manner as described above. As a result, the occurrence of a colored band corresponding to the polypeptide mentioned above was visually conformed. This fact indicates that the Escherichia coli carrying the plasmid pCPN533a expressed the 53K antigenic polypeptide capable of reacting with a monoclonal antibody specifically reactive with Chlamydia pneumoniae.

Example 3: Acquisition of DNA coding for the entire 53KDa antigenic polypeptide of Chlamydia pneumoniae

A DNA possessing base sequences of SEQ ID Nos. 26 and 27 was synthesized based on the base sequenc of SEQ ID No. 9 by the use of a DNA synthesizing device.

Ten (10) µl of the aqueous solution of genome DNA of the Chlamydia pneumoniae YK 41 strain (DNA content: about 1 µg) obtained in Example 1 and 5 µl of a K buffer concentrated to 1/10 times the original v lume, 35 µl of purified water, and 5 µl of a limiting enzyme Hind III (19 U/µl) added thereto were kept together at 37°C for three hours.

The resultant reaction solution was extracted from phenol. The extract and ethanol added thereto were together

centrifuged to obtain a precipitate. This precipitate and 5 μl of the Hind III cassette DNA (20 ng/μl) in the PCR in vitro Cloning Kit (proprietary designation of Takara Shuzo Co., Ltd.) and 15 μl of ligation solution added thereto were kept together at 16°C for 30 minutes.

The resultant reaction solution was extracted from phenol. The extract and ethanol added thereto are centrifuged together to acquire a precipitate. This precipitate was dissolved in 10 μl of purified water.

The resultant solution and 78.5 μl of purified water, 10 μl of a PCR grade buffer concentrated to 1/10 times the original volume, 8 μl of 2.5 mM dNTP, and 0.5 μl (5 U/μl) of Taq polymerase added thereto and 1 μl of a DNA possessing the base sequence of SEQ ID No. 26 (20 pmol/μl) and 1 μl of a DNA possessing the base sequence of SED ID No. 28 (20 pmol/μl) (enclosed as Primer CI in the aforementioned kit) further added thereto as primer DNA's were placed together in a microtube, 0.6 ml in volume, with two drops of mineral oil superposed on the resultant mixture in the microtube. The mixture was subjected to 30 temperature cycles each consisting of 30 seconds at 94°C, 2 minutes at 55°C, and 3 minutes at 72°C. This procedure will be referred to hereinafter as "PCR process."

One (1) μl of the reaction solution resulting from the PCR process and 1 μl of a DNA possessing the base sequence of SEQ ID No. 27 (20 pmol/μl) and 1 μl of a DNA possessing the base sequence of SED ID No. 29 (20 pmol/μl) (enclosed as Primer C2 in the aforementioned kit) added thereto as primer DNA's were subjected to the PCR process.

The reaction solution resulting from the second PCR process was subjected to electrophoresis with 1.2% low melting agarose gel to separate an agarose gel containing a DNA, about 1.4 kbp in size. The Wizard PCR Prep kit (Promega Corp) was used for the purification of the DNA. The separated agarose gel and the buffer solution enclosed in the kit were together heated to dissolve the agarose gel. The purifying resin enclosed in the kit was added to the resultant solution to adsorb the DNA. The resultant mixture was centrifuged to obtain the purifying resin as a precipitate. The precipitate was washed with propanol and centrifuged again to obtain a precipitate. Purifying water was added to the precipitate to dissolve the DNA out of the purifying resin. The resultant mixture was centrifuged to obtain a supernatant (aqueous DNA solution). The process described above will be referred to herein below as "DNA purifying process."

The acquired aqueous DNA solution was caused to undergo a sequence reaction by the fluorescence-labeled terminator sequence method using the Taq DNA polymerase templated by the contained DNA and was analyzed for the base sequence of DNA with a DNA sequencer, Model 373A, (Applied Biosystems Corp.). The DNA base sequence consequently obtained was compiled and ligated by the software for gene sequence analysis (produced by Hitachi Software Engineering Co., Ltd. and marketed under trademark designation of "DNASIS") to estimate the amino acid translation region. The process just described will be referred to herein below as "base sequence analyzing process."

When the acquired DNA was analyzed for base sequence, it was found that this DNA possessed about 50 bp of base sequences on the 3' terminal side of the DNA encoding the antigen polypeptide of Chlamydia pneumoniae acquired in Example 1. It was further found that about 0.7 kb of coding region containing a stop codon existed on the downstream side of the base sequence.

A DNA possessing the base sequence of SEQ ID No. 30 was synthesized as a primer corresponding to the upstream part of the DNA encoding the antigen polypeptide of Chlamydia pneumoniae based on the base sequence of SEQ ID No. 9 and a DNA possessing the base sequence of SEQ ID No. 31 was synthesized as a primer corresponding to the downstream part of the DNA encoding the antigen polypeptide of Chlamydia pneumoniae based on the base sequence containing the aforementioned about 0.7 kb of code zone severally by the use of the DNA synthesizer.

The PCR process was performed on 1 μl of the DNA possessing the base sequence of SEQ ID No. 30 DNA and 1 μl of the DNA possessing the base sequence of SEQ ID No. 31 as a primer DNA by using 1 μl of the aqueous solution of the genome DNA of the Chlamydia pneumoniae YK 41 strain obtained in Example 1.

The DNA purifying process mentioned above was carried out on the reaction solution resulting from the third round of the PCR process to obtain about 1.5 kbp of DNA.

The base sequence analyzing process mentioned above was carried out on the acquired aqueous solution of DNA.

When the base sequence of the acquired DNA was analyzed, it was found that this DNA possessed the base sequence of SEQ ID No. 3 and encoded the amino acid sequence of SEQ ID No. 1.

DNA coding for the entire 53KDa antigenic polypeptide of Chlamydia pneumoniae was obtained by effecting a genome walking by the use of the plasmid pCPN533a and the DNA library of λ gtII.

Example 4: Preparation of recombinant vector containing DNA coding for entire 53KDa antigenic polypeptide of Chlamydia pneumoniae and preparation of transformant carrying the vector

The recombination vector containing the DNA coding for the whole Chlamydia pneumoniae 53 kDa antigen polypeptide and the transformant containing the vector can be manufactured as follows.

A recombinant vector containing a DNA coding for the entire 53KDa antigenic polypeptide of Chlamydia pneumoniae and a transformant carrying the vector are prepared by following the procedure of Exampl 2 using the DNA coding for the entire 53KDa antigenic polypeptide of Chlamydia pneumoniae.

Example 5: Preparation of DNA coding for 73K antigenic polypeptide of Chlamydia pneumoniae

A hybridoma 70 was acquired by the same method as used for the acquisition of a hybridoma AY6E2E8. Th murine ascites was acquired by using the hybridoma 70. The supernatant of the ascites was analyzed for the quality of the monoclonal antibody contained therein. The results of this analysis indicate that this monoclonal antibody was specific to the antigen polypeptide of 73 KDa of Chlamydia pneumoniae.

A clone 70-2S λ phage was obtained by following the procedure of Example 1 while using a monoclonal antibody 70 in the place of the monoclonal antibody SCP53 or AY6E2E8. From the phage, a sequence of SEQ ID No: 13 was obtained.

The results of the analysis of the sequence of SEQ ID No: 13 clearly indicate that about 90% of the amino acid sequence of the 73K antigenic protein of Chlamydia pneumoniae from the N terminal toward the C terminal thereof was clarified.

The search for homology of both the base sequence and the amino acid sequence of SEQ ID No: 13 was effected in accordance with the GenBank data base. The results of the search clearly show that these sequences exhibited high homology with the gene base sequence isolated from Chlamydia trachomatis [L. M. Sardinia et al: J. Bacteriol., Vol. 17., 335-341 (1989)].

Example 6: Production of anti-Chlamydia pneumoniae antibody using antigenic polypeptide of Chlamydia pneumoniae as antigen

The anti-Chlamydia pneumoniae antibody can be produced by using the antigen polypeptide of Chlamydia pneumoniae as follows.

(A) Culture and passage of myeloma cell strain

As a myeloma cell strain, P3X63Ag8.653 (ATCC CRL-1580) is cultured and passed in a RPMI1640 culture medium containing 10% (v/v) bovine fetal serum. Two weeks before the strain is subjected to cellular fusion, this strain is cultured for one week in the RPMI1640 culture medium containing 0.13 mM of 8-azaguanine, 0.5 μg/ml of a mycoplasma removing agent (produced by Dainippon Pharmaceutical Co., Ltd. and marketed under product code of "MC-210"), and 10% (v/v) bovine fetal serum. The subsequent one week is spent for culture in an ordinary culture medium.

(B) Immunization of mouse

The amount 200 μl of a solution of the antigenic polypeptide mentioned above and having a protein concentration of 270 μg/ml is emulsified by addition of 200 μl of a Freund's complete adjuvant. The produced emulsion is hypodermically injected in an amount of 150 μl into the back of a mouse (the date of this injection reckoned as 0th day). On the 14th day, 34th day, and 49th day, 100 μl of a suspension of the antigenic polypeptide having a protein concentration of 270 μg/ml is intraabdominally injected into the mouse. Further, 50 μl of a suspension of the same antigenic polypeptide having a protein concentration of 800 μg/ml is intraabdominally injected into the mouse on the 69th day and 100 μl of the same suspension injected intraabdominally to the mouse on the 92nd day. On the 95th day, the mouse is sacrificed to extract the spleen. This spleen is utilized for cellular fusion.

(C) Cellular fusion

In a round-bottom glass tube, 10^8 splenic cells obtained from the spleen mentioned above and 10^7 myeloma cells are thoroughly mixed. The resultant mixture is centrifuged at 1,400 rpm for five minutes and, with the consequently formed supernatant removed therefrom, further mixed thoroughly. The produced mixture is added to 0.4 ml of a RPMI1640 culture medium containing 30% (w/v) polyethylene glycol and kept warmed in advance at 37 °C and left standing therein for 30 seconds. The culture medium now containing the mixture is centrifuged at 700 rpm for six minutes. The glass tube, after adding 10 ml of the RPMI1640 culture medium, is gently rotated so as to permit thorough mixtur of the polyethylene glycol. The mixture is then centrifuged at 1,400 rpm for five minutes. The supernatant consequently formed is thoroughly removed. The sediment and 6 ml of the HAT culture medium added thereto are left standing for five minutes. The resultant mixture and 10 to 20 ml of the HAT culture medium added thereto are left standing for 30 minutes. The HAT culture medium is further added thereto in such an amount as to set a myeloma cell concentration at 3.3 x 10^5/ml to obtain a suspension of cells. The suspension is dispensed at a rate f two drops to each of the 96-well plastic culture vessel by the use of a Pasteur pipet. The suspension is cultured under an ambience of 5% (v/v) carbon dioxide gas at 36 °C. Then, one or two drops f the HAT culture medium are added to each of the wells after the elapse of one day, seven days, and 14 days.

(D) Screening of antibody-producing cells

The antigenic polypeptide mentioned above is suspended in a 0.05M sodium bicarbonate suspension (pH 9.6) containing 0.02% (w/v) sodium azide so as to set the protein concentration in the range of from 1 to 10 μg/ml. The resultant suspension is dialyzed against a 0.05M sodium bicarbonate buffer (pH 9.6) containing 0.02% of sodium azide. The dialyzate is diluted so as to set the protein concentration in the range of from 1 to 10 μg/ml. The diluted dialyzate is dispensed at a rate of 50 μl to each of the wells of a 96-well plate for EIA made of vinylchloride and left standing therein at 4 °C overnight to effect adsorption of the antigen. The supernatant consequently formed is removed from the wells. To ach of the wells, 150 μl of PBS containing 0.02% (w/v) Tween 20 is added, left standing therein for three minutes, then removed, and washed. The washing is repeated once more. To the well, 100 μl of PBS containing 1% (v/v) bovine serum albumin is added and left standing at 4 °C overnight to effect blocking. The PBS containing the bovine serum albumin is removed and then washed twice more with the PBS containing 0.02% (w/v) Tween 20 in the same manner as described above. Then, 50 μl of the culture supernatant of fused cells is added to the well and left standing therein at room temperature for two hours. The well is washed three times with the PBS containing 0.02% (w/v) Tween 20 in the same manner as described above. In the well, 50 μl of a goat anti-mouse IgG antibody labelled with peroxidase (25 ng/ml) is placed and left standing at room temperature. The well is washed three times with the PBS containing 0.02% (w/v) Tween 20 in the same manner as described above. In the well, 50 μl of an ABTS solution (produced by KPL Corp.) is placed and left standing at room temperature for 15 minutes to one hour to effect a reaction of coloration. The culture solution in the well is tested for absorbance at 405 nm with the photometer for 96-well EIA plate. The cells in the positive wells are severally recovered with the Pasteur pipet, transferred into a 24-well plastic culture vessel and, after adding 1 to 2 ml of the HAT culture medium, cultured in the same manner as described above.

(E) Cloning by limiting dilution method

The fused cells of two strains propagated in a 24-well plastic culture vessel are tested for cell concentration and severally diluted with a HT culture medium until the number of cells decreased to 20/ml. Separately, the thymocytes of four- to six-weeks old mice suspended in the HT culture medium are dispensed at a rate of 1 to 2 x 10^5/well to a 96-well plastic culture vessel and the fused cells mentioned above (cell concentration 20/ml) are dispensed at a rate of 50 μl/well to the same culture vessel and cultured under an ambience of 5% (v/v) carbon dioxide gas at 36 °C. One day, seven days, and 14 days thereafter, the HT culture medium is added thereto at a rate of one to two drops per well. From ach of the wells in which the growth of cells is observed, the culture supernatant is recovered in a fixed amount of 50 μl. This supernatant is analyzed in the same manner as in (D) titled "Screening of antibody-producing cells" to confirm the production of an antibody therein.

The cells which allowed the occurrence of a single cellular colony in a well, produced an antibody capable of reacting with an elementary body, and achieved quick proliferation are recovered from the relevant wells and are subsequently proliferated in a 24-well plastic culture vessel. Further, a hybridoma producing an anti-Chlamydia pneumoniae antibody is obtained by repeating the same cloning process as described above. This hybridoma is cultured and the anti-Chlamydia pneumoniae antibody is produced from the resultant culture supernatant.

Example 7: Detection and determination of anti-Chlamydia pneumoniae antibody using an antigenic polypeptide as an antigen

The anti-Chlamydia pneumoniae antibody can be detected and measured by using the antigen polypeptide of this invention as an antigen as follows.

The polypeptide formed of the amino acid sequence of SEQ ID No: 1 is used as an antigenic polypeptide. It is fixed on a microtiter plate, made to add a PBS containing bovine serum albumin, and left standing overnight at 4 °C to effect blocking. The PBS containing the bovine serum albumin was removed and the well is washed twice with the PBS containing 0.02% (w/v) Tween 20. The blood serum from a patient is added to the well thereto and is left standing at room temperature for two hours. The resultant solution is removed and the well is washed three times with the PBS containing 0.02% (w/v) Tween 20 in the same manner as described above. In each of the wells, a peroxidase-labelled mouse anti-human IgG antibody is placed and left standing at room temperature for two hours. The solution in the well is removed and the well is washed three times with the PBS containing 0.02% (w/v) Tween 20 in the same manner as described above. In the well, an ABTS solution (produced by KPL Corp.) is placed and left standing at room temperature for 15 minutes to one hour to effect a reaction of coloration. The solution is then tested for absorbanc at 405 nm by the use f a photometer for 96-well EIA plate.

Exampl 8: Production of recombinant vector carrying DNA coding for fused protein of peptide containing DHFR and part of antigenic polypeptide of Chlamydia pneumoniae and production of transformant containing the recombinant vector

A plasmid pBBK10MM was severed with restriction enzymes of BamHI and XhoI and subjected to 1.2% low melting temperature solution agarose gel electrophoresis to excise about 4.6 Kbp of DNA fragment. This fragment was purified.

Separately, a 53-3S λ phage DNA was severed with a restriction enzyme EcoRI to obtain about 1.0 Kbp of DNA fragment similarly in a purified form. This DNA segment was further severed with a restriction enzyme AvaII to obtain about 0.8 Kbp of a DNA segment similarly in a purified form. The amount 100 ng of about 4.6 Kbp of DNA segment, 100 ng of about 0.8 Kbp of DNA segment mentioned above, and 1 ng of each of the synthetic DNA's of SEQ ID Nos: 21 through 24 added thereto were subjected to DNA ligation by the use of the DNA ligation kit (produced by Takara Shuzo Co., Ltd.). The reaction product was placed in an Escherichia coli HB101 strain competent cell (produced by Takara Shuzo Co., Ltd.) to produce a transformant.

This transformant was spread on a LB agar culture medium containing 50 mg/L of ampicillin and cultured thereon at 37 °C for 24 hours. The Escherichia coli colony consequently obtained was inoculated to 3 ml of the LB culture medium containing 50 mg/L of ampicillin and then shaken cultured overnight at 37 °C. The plasmid vector was separated from the culture medium by the alkali lysis method, severed with a restriction enzyme NruI, and analyzed by 0.8% agarose gel electrophoresis to select an Escherichia coli possessing a recombinant plasmid vector which had produced DNA segments of 616 bp and 4822 bp. The recombinant plasmid vector thus obtained was designated as pCPN533T. This plasmid vector was a DNA of a length of about 5.4 kbp possessing a base sequence of SEQ ID No: 25. It was capable of expressing a fused protein having a polypeptide containing part of the 53KDa antigenic polypeptide of Chlamydia pneumoniae ligated to the C terminal of DHFR. The base sequence of the DNA coding for this fused protein was shown by SEQ ID No: 18. The amino acid sequence deduced from this base sequence was shown by SEQ ID No: 16.

Example 9: Recognition of fused protein of polypeptide containing DHFR and part of 53KDa antigenic polypeptide of Chlamydia pneumoniae

One platinum loop full of the HB101 strain of Escherichia coli retaining plasmid pCPN533T was inoculated to 3 ml of the LB culture medium containing 50 mg/l of ampicillin and shaken cultured overnight at 37°C. The amount 10 µl of the culture medium containing the Escherichia coli and 10 µl of loading buffer (a 0.156M tris-hydrochloride buffer containing 0.01% of bromophenol blue, 10% of mercapto ethanol, 20% of glycerol, and 5% of SDS and having pH 6.8) added thereto were heated at 80 °C for five minutes. The resultant reaction solution was subjected to 5-20% polyacrylamide gradient gel electrophoresis. On the anode plate of a semi-dry blotting device, one filter paper wetted with a 0.3M tris aqueous solution containing 10% of methanol and 0.05% sodium dodecyl sulfate, one filter paper wetted with a 25 mM tris aqueous solution containing 10% of methanol and 0.05% of sodium dodecyl sulfate, one filter paper wetted with a 25 mM tris aqueous solution containing 10% of methanol and 0.05% of sodium dodecyl sulfate, one nitrocellulose membrane wetted with a 25 mM tris aqueous solution containing 10% of methanol, 0.05% of sodium dodecyl sulfate, and 40 mM aminocaproic acid, the polyacryl amide gel completely undergone the aforementioned electrophoresis and two filter papers wetted with a 25 mM tris aqueous solution containing 40 mM aminocaproic acid were superposed sequentially in the order mentioned. A cathode plate was set as opposed to the anode plate across the superposed filters and an electric current was passed through the filters at a current density of 2.5 mA/cm^2 for one hour to effect transfer of the protein in the polyacrylamide gel to the nitrocellulose membrane. The nitrocellulose membrane was placed in a TBS buffer containing 0.1% of bovine serum albumin and left standing therein at room temperature for not less than one hour to effect blocking. The nitrocellulose membrane was washed twice with the TTBS buffer and then shaken in a monoclonal antibody solution produced by the hybridoma SCP53 (in the 5 to 10 µg/ml TTBS buffer) at 37 °C for one hour. The nitrocellulose membrane was washed three times with the TTBS buffer and then shaken in an aqueous solution of an anti-mouse IgG antibody labelled with peroxidase (in the 50 ng/ml TTBS buffer) at 37 °C for one hour. The nitrocellulose membrane was washed three times with the TTBS buffer and then placed in a coloring ground substance solution (obtained by mixing 100 ml of the TBS buffer with 60 µl of an aqueous 30% hydrogen peroxide solution, and 20 ml of a methanolic solution of 4-chloro-1-naphthol) and left reacting at room temperature for 30 minutes. The nitrocellulose membrane was extracted, washed with purified water, and then air-dried. As a result, colored bands were observed at positions corresponding to sizes of fused protein. This fact indicates that the Escherichia coli possessing the plasmid pCPN533T expressed the fusion protein containing 53KDa antigen capable of reacting with the monoclonal antibody specifically reacting Chlamydia pneumoniae.

Exampl 10: Acquisition of DNA coding for entire 53KDa antigenic polypeptide of Chlamydia pneumoniae

The DNA encoding the whole 53 kDa antigen polypeptide of Chlamydia pneumoniae was already acquired in

Example 3. However, it was separately obtained the DNA as follows.

A DNA coding for the entire 53KDa antigenic polypeptide of Chlamydia pneumoniae was also obtained by effecting a genome walking by the use of the plasmid pCPN533T and the DNA library of λ gtII. When these DNAs were analyzed for base sequence, it was found to possess the 484th through 1947th base sequences of SEQ ID No: 17 and code for the 162nd through 649th amino sequences of SEQ ID No: 15.

Example 11: Production of recombinant vector carrying DNA coding for fused protein of DHFR and entire 53KDa antigenic polypeptide of Chlamydia pneumoniae and production of transformant containing the recombinant vector

The recombinant vector containing the DNA encoding the fused protein of DHFR and the whole 53 kDa antigen polypeptide of Chlamydia pneumoniae and the transformant containing the recombinant vector can be produced as follows.

A recombinant vector containing a DNA coding for the fused protein of the DHFR and the entire 53KDa antigenic polypeptide of Chlamydia pneumoniae is produced by following the procedure of Example 8 while using a DNA coding for the plasmid pBBK10MM and the entire 53KDa antigenic polypeptide of Chlamydia pneumoniae mentioned above and th transformant containing the recombinant vector was produced. The base sequence of the DNA coding for the fused protein is shown by SEQ ID No: 17 and the amino acid sequence deduced from this base sequence is shown by SEQ ID No: 15.

Example 12: Production of anti-Chlamydia pneumoniae antibody by use of fused protein as an antigen

The anti-Chlamydia pneumoniae antibody can be produced by using the fused protein of this invention as an antigen as follows.

A hybridoma producing an anti-Chlamydia pneumoniae antibody is obtained by following the procedure of Example 6 while using the fused protein mentioned above as an antigen for immunization. This hybridoma is cultured and the anti-Chlamydia pneumoniae antibody is produced from the culture supernatant consequently formed.

Example 13: Detection and determination of anti-Chlamydia pneumoniae antibody by using fused protein as antigen

The anti-Chlamydia pneumoniae can be detected and measured by using the fused protein of this invention as an antigen as follows.

The polypeptide formed of the amino acid sequence of SEQ ID No: 15 is used as a fused protein. It is fixed on a microtiter plate, made to add a PBS containing bovine serum albumin, and left standing overnight at 4 °C to effect blocking. The PBS containing the bovine serum albumin is removed and the plate is washed twice with the PBS containing 0.02% (w/v) Tween 20. The blood serum from a patient is added to the wells and is left standing at room temperature for two hours. The well is washed three times with the PBS containing 0.02% (w/v) Tween 20 in the same manner as described above. In each of the wells, a peroxidase-labelled mouse anti-human IgG antibody is placed and left standing at room temperature for two hours. The culture solution in the well is washed three times with the PBS containing 0.02% (w/v) Tween 20 in the same manner as described above. In the well, an ABTS solution (produced by KPL Corp.) is placed and left standing at room temperature for 15 minutes to one hour to effect a reaction of coloration. The culture solution is then tested for absorbance at 405 nm by the use of a photometer for 96-well EIA plate.

Example 14: Detection of Chlamydia pneumoniae gene by PCR method

A DNA formed of a base sequence of SEQ ID No: 19 and a DNA formed of a base sequence of SEQ ID No: 20 were chemically synthesized with a DNA synthesizing device produced by Applied Biosystems Corp and were designated respectively as Primer 53F2 and Primer 53R2.

The cells infected with the YK41 strain of Chlamydia pneumoniae or the L2 strain of Chlamydia trachomatis or the Bugd. 17-SL strain of Chlamydia psittaci were recovered by centrifugation. The cells plus 0.1 ml of a 50 mM tris-hydrochloride buffer (pH 8.3) containing 50 mM of KCl, 2.5 mM of $MgCl_2$, 0.1 mg/ml of gelatin, 0.45% of Nonidet P40, 0.45% of Tw en 20, and 0.1 mg/ml of proteinase K were kept warmed at 56 °C for one hour and then heated at 95 °C for 10 minutes to inactivate the proteinase K and obtain a sample containing the gene of relevant chlamydia.

One (1) µl of the sample was combined with 78.5 µl of purified water, 8 µl of an aqueous 2.5 mM dNTP solution, 10 µl of a 100 mM tris-hydr chloride buffer (pH 8.3) containing 500 mM of KCl and 15 mM of $MgCl_2$, 1 µl each of the aqueous solutions of 30 µM Primer 53F2 and Primer 53R2 mentioned above, and 0.5 µl of 5 U/µl of Taq polymerase. The resultant mixture was superposed by 50 µl of mineral oil and subjected to 30 cycles of a procedure which consisted of heating at 94 °C for 30 seconds, at 60 °C for 30 seconds, and at 72 °C for 60 seconds, cooling, and warming.

After the reaction was completed, 2 µl of the reaction solution was subjected to agarose gel electrophoresis, with the gel immersed in 0.5 µ/ml of ethidium bromide to make a band of DNA visible by irradiation of an ultraviolet light.

As a result, the sample obtained from the YK41 strain of Chlamydia pneumoniae was found to form a visible band of DNA of a size of 360 bp corresponding to a region interposed between the base sequence of Primer 53F2 and a base sequence complementary to the base sequence of Primer 53R2 in all the base sequences of SEQ ID No: 3. The samples obtained from the other strains wer not found to form any visible band of DNA.

INDUSTRIAL APPLICABILITY

The antigenic polypeptide of this invention formed of a polypeptide A containing at least five continuous amino acid sequences in the polypeptides of SEQ ID No: 1 can be utilized as for the examination of an antibody of Chlamydia pneumoniae.

The antigenic polypeptide of this invention the polypeptide A of which is a polypeptide arising from the loss of 1 to 250 amino acids from the polypeptides of SEQ ID No: 1 has an amino acid sequence of a small length and, therefore, is enabled to increase the number of antigenic peptides which can be fixed as on a carrier. Thus, it can be utilized for the production of a diagnostic agent of high sensitivity.

The antigenic polypeptide of this invention the polypeptide A of which is a polypeptide resulting from the substitution of 1 to 100 amino acids in the polypeptides of SEQ ID No: 1 by other amino acids is capable of forming a structure only sparingly susceptible of the decomposition by a protease and, therefore, is excellent in stability as an antigen.

The antigenic polypeptide of this invention the polypeptide A of which is a polypeptide having an amino acid or 2 to 1000 amino acid sequences ligated to at least five continuous amino acid sequences in the polypeptides of SEQ ID No: 1 can be fixed as to a carrier by making use of the amino acid or 2 to 1000 amino acid sequences and, therefore, does not easily yield to decline or loss of the antigenecity by fixation.

The antigenic polypeptide of this invention the polypeptide A of which is a polypeptide formed of amino acid sequences of SEQ ID No: 1 possesses the whole of antigenic polypeptides specific to Chlamydia pneumoniae and, therefore, is highly suitable for the examination of antigens and for accurate diagnosis of infections involving Chlamydia pneumoniae.

The antigenic polypeptide of this invention the polypeptide A of which is a polypeptide formed of amino acid sequences of SEQ ID No: 2 or ID No: 5 possesses an antigenic part specific to Chlamydia pneumoniae and, therefore, is highly suitable for the examination of antigens and for accurate diagnosis of infections involving Chlamydia pneumoniae.

The DNA of this invention which is a DNA coding for any of the antigenic polypeptides mentioned above or a DNA complementary thereto can be utilized for the production of an antigenic polypeptide suitable for the examination of antigens of Chlamydia pneumoniae, the diagnosis of infections involving Chlamydia pneumoniae, and the like.

The DNA of this invention the base sequence of which is a base sequence of SEQ ID No: 3 codes for the whole of the antigenic polypeptide specific to Chlamydia pneumoniae can be utilized for the production of an antigenic polypeptide suitable for the examination of antibodies specific to Chlamydia pneumoniae.

The DNA of this invention the base sequence of which is a base sequence of SEQ ID No: 4 or ID No: 7 codes for the antigenic part specific to Chlamydia pneumoniae can be utilized for the production of an antigenic polypeptide suitable for the examination of antigens specific to Chlamydia pneumoniae.

The recombinant vector of this invention containing any of the DNA's mentioned above can be utilized for the production of an antigenic polypeptide suitable for the examination of an antibody of Chlamydia pneumoniae and the diagnosis of infections involving Chlamydia pneumoniae.

The recombinant vector of this invention which is a pCPN533a plasmid possessing a base sequence of SEQ ID No: 10 is capable of expressing a polypeptide possessing an antigenic part specific to Chlamydia pneumoniae and, therefore, can be utilized for the production of an antigenic polypeptide highly suitable as for the examination of antibodies specific to Chlamydia pneumoniae.

The transformant of this invention which contains any of the recombinant vectors mentioned above can be utilized for the production of an antigenic polypeptide suitable as for the examination of antibody specific to Chlamydia pneumoniae.

The method of this invention for the production of an anti-Chlamydia pneumoniae antibody which is characterized by using any of the antigenic polypeptides mentioned above as an antigen can be utilized for the production of a diagnostic agent for infections involving Chlamydia pneumoniae.

The method of this invention for the detection and determination of an anti-Chlamydia pneumoniae antibody which is characterized by using any of the antigenic polypeptides mentioned above as an antigen can be utilized for the examination of antibodies of Chlamydia pneumoniae and the diagnosis of infections involving Chlamydia pneumoniae.

Particularly when an antigenic polypeptide having an amino acid sequence of a small length is utilized, it manifests high sensitivity because it allows an increase in the number of antigenic polypeptides to be fixed as on a carrier.

When an antigenic polypeptide having amino acids inherent therein substituted by other amino acids is utilized for the detection and determination mentioned above, the results of the detection and determination are highly reliable because the antigenic polypeptide is capable of forming a structure only sparingly susceptible to decomposition by a

protease and, consequently, excellent in stability.

When an antigenic polypeptide adding other amino acid sequences is utilized for the diagnosis of infections involving Chlamydia pneumoniae, it fulfills the role ideally because it enables a polypeptide being used as an antigen to be fixed as on a carrier by making use of amino acids or 2 to 1000 amino acid sequences and only sparingly incurs decline or loss of the antigenicity due to the fixation.

When an antigenic polypeptide formed of amino acid sequences of SEQ ID No: 1 is utilized for the examination of antibodies or the diagnosis of infections involving Chlamydia pneumoniae, it fulfills the examination or the diagnosis with perfect accuracy because a polypeptide being used as an antigen possesses the whole antigenic polypeptide specific to Chlamydia pneumoniae.

When an antigenic polypeptide formed of amino acid sequences of SEQ ID No: 2 or ID No: 5 is utilized for the examination of antibodies or the diagnosis of infections involving Chlamydia pneumoniae, it fulfills the examination or the diagnosis with perfect accuracy because a polypeptide being used as an antigen possesses an antigenic part specific to Chlamydia pneumoniae.

The reagent of this invention for the detection and determination of an anti-Chlamydia pneumoniae antibody which contains any of the antigenic polypeptides mentioned above as an antigen ideally fits the examination of antibodies of Chlamydia pneumoniae and the diagnosis of infections involving Chlamydia pneumoniae.

Particularly, when an antigenic polypeptide having an amino acid sequence of a small length is utilized for the reagent, the reagent enjoys high sensitivity because it allows an increase in the number of antigenic polypeptides to be fixed as on a carrier.

When an antigenic polypeptide having amino acids inherent therein substituted by other amino acids is utilized for the detection and determination mentioned above, the results of the examination and determination are highly reliable because the antigenic polypeptide is capable of forming a structure only sparingly susceptible to decomposition by a protease and, as a result, excellent in stability.

Further, when an antigenic polypeptide adding other amino acid sequences is utilized for the diagnosis of infections involving Chlamydia pneumoniae, it fulfills the role ideally because it enables a polypeptide being used as an antigen to be fixed as on a carrier by making use of amino acids or 2 to 1000 amino acid sequences and only sparingly incurs decline or loss of the antigenicity due to the fixation.

Then, when an antigenic polypeptide formed of amino acid sequences of SEQ ID No: 1 is utilized for the examination of antibodies or the diagnosis of infections involving Chlamydia pneumoniae, it fulfills the examination or the diagnosis with perfect accuracy because a polypeptide being used as an antigen possesses the whole antigenic polypeptide specific to Chlamydia pneumoniae.

Wh n an antigenic polypeptide formed of amino acid sequences of SEQ ID No: 2 or ID No: 5 is utilized for the examination of antibodies or the diagnosis of infections involving Chlamydia pneumoniae, it fulfills the examination or the diagnosis with perfect accuracy because a polypeptide being used as an antigen possesses an antigenic part specific to Chlamydia pneumoniae.

The diagnostic agent of this invention which has any of the antigenic polypeptides mentioned above as an active component ideally fits the diagnosis of infections involving Chlamydia pneumoniae.

Particularly, when an antigenic polypeptide having an amino acid sequence of a short length is adopted for the agent, the agent enjoys high sensitivity because it allows an increase in the number of antigenic polypeptides to be fixed as on a carrier.

When an antigenic polypeptide having amino acids inherent therein substituted by other amino acids is utilized for the detection and determination mentioned above, the results of the examination and determination are highly reliable because the antigenic polypeptide is capable of forming a structure only sparingly susceptible to decomposition by a protease and, as a result, excellent in stability.

Further, when an antigenic polypeptide adding other amino acid sequences is utilized for the diagnosis of infections involving Chlamydia pneumoniae, it fulfills the role ideally because it enables a polypeptide being used as an antigen to be fixed as on a carrier by making use of amino acids or 2 to 1000 amino acid sequences and only sparingly incurs decline or loss of the antigenicity due to the fixation.

Then, when an antigenic polypeptide formed of amino acid sequences of SEQ ID No: 1 is utilized for the examination of antibodies or the diagnosis of infections involving Chlamydia pneumoniae, it fulfills the examination or the diagnosis with perfect accuracy because a polypeptide being used as an antigen possesses the whole antigenic polypeptide specific to Chlamydia pneumoniae.

When an antigenic polypeptide formed of amino acid sequences of SEQ ID No: 2 or ID No: 5 is utilized for the examination of antibodies or the diagnosis of infections involving Chlamydia pneumoniae, it fulfills the examination or th diagnosis with perfect accuracy because a polypeptide being used as an antigen possesses an antigenic part specific to Chlamydia pneumoniae.

The fused protein of this invention which has ligated to a polypeptide of SEQ ID No: 14 either directly or through the medium of an amino acid sequence a polypeptide A containing at least five continuous amino acid sequences in the polypeptides of SEQ ID No: 1 can be utilized as for the examination of antibodies of Chlamydia pneumoniae.

The fused protein of this invention the polypeptide A of which is a polypeptide arising from the loss of 1 to 250 amino acids from the polypeptides of SEQ ID No: 1 has an amino acid sequence of a small length and, therefore, is enabled to increase the number of antigenic peptides which can be fixed as on a carrier. Thus, it can be utilized for the production of a diagnostic agent of high sensitivity.

The fused protein of this invention the polypeptide A of which is a polypeptide resulting from the substitution of 1 to 100 amino acids in the polypeptides of SEQ ID No: 1 by other amino acids is capable of forming a structure only sparingly susceptible of the decomposition by a protease and, therefore, is excellent in stability as an antigen.

The fused protein of this invention which is a polypeptide formed of amino acid sequences of SEQ ID No: 15 is highly suitable for the examination of antibodies and the diagnosis of infections involving Chlamydia pneumoniae because it possesses the whole of antigenic polypeptides specific to Chlamydia pneumoniae.

The fused protein of this invention which is a polypeptide formed of amino acid sequences of SEQ ID No: 16 is highly suitable for the examination of antibodies and the diagnosis of infections involving Chlamydia pneumoniae because it possesses an antigenic part specific to Chlamydia pneumoniae.

The DNA of this invention which is a DNA coding for any of the fused proteins mentioned above or a DNA complementary thereto can be utilized for the production of a fused protein suitable for the examination of antibodies of Chlamydia pneumoniae, the diagnosis of infections involving Chlamydia pneumoniae, and the like.

The DNA of this invention the base sequences of which are base sequences of SEQ ID No: 17 can be utilized for the production of a fused protein suitable as for the examination of antibodies specific to Chlamydia pneumoniae because the fused protein coded for by this DNA possesses the whole of antigenic polypeptides specific to Chlamydia pneumoniae.

The DNA of this invention the base sequences of which are base sequences of SEQ ID No: 18 can be utilized for the production of a fused protein suitable as for the examination of antibodies specific to Chlamydia pneumoniae because the fused protein coded for by this DNA possesses an antigenic part specific to Chlamydia pneumoniae.

The recombinant vector of this invention which carries any of the DNA's mentioned above can be utilized for the production of a fused protein suitable for the examination of antibodies of Chlamydia pneumoniae and the diagnosis of infections involving Chlamydia pneumoniae.

The recombinant vector of this invention which is a pCPN533T plasmid can be utilized for the production of a fused protein highly suitable as for the examination of antibodies specific to Chlamydia pneumoniae because it is capable of expressing a fused protein possessing an antigenic part specific to Chlamydia pneumoniae.

The transformant of this invention which contains any of the recombinant vectors mentioned above can be utilized for the production of a fused protein suitable as for the examination of antibodies specific to Chlamydia pneumoniae.

The method of this invention for the production of an anti-Chlamydia pneumoniae antibody which is characterized by using any of the fused proteins mentioned above as an antigen can be utilized for the production of a diagnostic agent for infections involving Chlamydia pneumoniae.

The method of this invention for the detection and determination of an anti-Chlamydia pneumoniae antibody which is characterized by using any of the fused proteins mentioned above as an antigen is suitable for the examination of antibodies of Chlamydia pneumoniae and the diagnosis of infections involving Chlamydia pneumoniae.

Particularly, when a fused protein having an amino acid sequence of a short length is adopted for the method, the method enjoys high sensitivity because this fused protein allows an increase in the number of antigenic polypeptides to be fixed as on a carrier.

When a fused protein having amino acids inherent therein substituted by other amino acids is utilized for the detection and determination mentioned above, the results of the examination and determination are highly reliable because the fused protein is capable of forming a structure only sparingly susceptible to decomposition by a protease and, as a result, excellent in stability.

A fused protein which is formed of amino acid sequences of SEQ ID No: 15 is highly suitable for the examination of antibodies and the diagnosis of infections involving Chlamydia pneumoniae because a fused protein being used as an antigen possesses the whole of antigenic polypeptides specific to Chlamydia pneumoniae.

A fused protein which is formed of amino acid sequences of SEQ ID No: 16 is highly suitable for the examination of antibodies and the diagnosis of infections involving Chlamydia pneumoniae because a fused protein being used as an antigen possesses an antigenic part specific to Chlamydia pneumoniae.

The reagent of this invention which contains any of the fused proteins mentioned above as an antigen is suitable for the examination of antibodies of Chlamydia pneumoniae and the diagnosis of infections involving Chlamydia pneumoniae.

Particularly, when a fused protein having an amino acid sequence of a small length is utilized for the reagent, the reagent enjoys high sensitivity because it allows an increase in the number of antigenic polypeptides to be fixed as on a carrier.

When a fused protein having amino acids inherent therein substituted by other amino acids is utilized for the detection and determination mentioned above, the results of the examination and determination are highly reliable because the fused protein is capable of forming a structure only sparingly susceptible to decomposition by a protease and, as a

result, excellent in stability.

A fused protein which is formed of amino acid sequences of SEQ ID No: 15 is highly suitable for the examination of antibodies and the diagnosis of infections involving Chlamydia pneumoniae because a fused protein being used as an antigen possesses the whole of antigenic polypeptides specific to Chlamydia pneumoniae.

A fused protein which is formed of amino acid sequences of SEQ ID No: 16 is highly suitable for the examination of antibodies and the diagnosis of infections involving Chlamydia pneumoniae because a fused protein being used as an antigen possesses an antigenic part specific to Chlamydia pneumoniae.

The diagnostic medicine of this invention having any of the fused proteins mentioned above as an active component thereof is suitable for the examination of antibodies of Chlamydia pneumoniae and the diagnosis of infections involving Chlamydia pneumoniae.

Particularly, when a fused protein having an amino acid sequence of a small length is utilized for the agent, the agent enjoys high sensitivity because it allows an increase in the number of antigenic polypeptides to be fixed as on a carrier.

When a fused protein having amino acids inherent therein substituted by other amino acids is utilized for the detection and determination mentioned above, the results of the examination and determination are highly reliable because the fused protein is capable of forming a structure only sparingly susceptible to decomposition by a protease and, as a result, xcellent in stability.

A fused protein which is formed of amino acid sequences of SEQ ID No: 15 is highly suitable for the examination of antibodies and the diagnosis of infections involving Chlamydia pneumoniae because a fused protein being used as an antigen possesses the whole of antigenic polypeptides specific to Chlamydia pneumoniae.

A fused protein which is formed of amino acid sequences of SEQ ID No: 16 is highly suitable for the examination of antibodies and the diagnosis of infections involving Chlamydia pneumoniae because a fused protein being used as an antigen possesses an antigenic part specific to Chlamydia pneumoniae.

The probe and the primer of this invention are suitable for the detection and determination of a Chlamydia pneumoniae gene and the diagnosis of infections involving Chlamydia pneumoniae.

Particularly, a probe and a primer which possesses base sequences of SEQ ID No: 19 or ID No: 20 can be utilized for accurate diagnosis of infections involving Chlamydia pneumoniae because they possess base sequences specific to Chlamydia pneumoniae.

The method of this invention for the detection and determination of a Chlamydia pneumoniae gene by the use of any of the probes or primers mentioned above is suitable for the diagnosis of infections involving Chlamydia pneumoniae.

The reagent of this invention for the detection and determination of a Chlamydia pneumoniae which contains any of the probes or the primers mentioned above is ideally suitable for the diagnosis of infections involving Chlamydia pneumoniae.

The diagnostic agent of this invention which has any of the probes or the primers mentioned above as an active component is ideally suitable for the diagnosis of infections involving Chlamydia pneumoniae.

Sequence Listing

INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:488 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile Met
 1               5                  10                  15
Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp Lys
            20                  25                  30
Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly Lys
        35                  40                  45
Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly Lys
    50                  55                  60
Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln Gly
65                  70                  75                  80
Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala Asp
                85                  90                  95
Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala Thr
            100                 105                 110
Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met Glu
        115                 120                 125
Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys Glu
    130                 135                 140
Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly Ser
145                 150                 155                 160
Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro Arg
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                165                 170                 175
Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln Thr
            180                 185                 190
Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr Gln
        195                 200                 205
Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala Ile
    210                 215                 220
Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala Glu
225                 230                 235                 240
Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr Val
                245                 250                 255
Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile Val Ala Ala
            260                 265                 270
Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala Gly Ala Ala
        275                 280                 285
Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala Ala Ala Thr
    290                 295                 300
Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln Ala Val Lys
305                 310                 315                 320
Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala Ala Ile Lys
                325                 330                 335
Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr Leu Val Lys
            340                 345                 350
Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val Phe Ala Lys
        355                 360                 365
Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser Lys Val Ile
    370                 375                 380
Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly Val Val Val
385                 390                 395                 400
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Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln Leu Ser Glu
405 410 415

Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly Lys Leu Gln
420 425 430

Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp Gln Gln Ala
435 440 445

Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu Met Thr Gln
450 455 460

Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr Ala Ala Ile
465 470 475 480

Ser Gly Ala Ile Ala Gly Ala Ala
485 488

INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:271 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile Met
1 5 10 15

Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp Lys
20 25 30

Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly Lys
35 40 45

Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly Lys
50 55 60

Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln Gly

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 65                  70                  75                  80
Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala Asp
                 85                  90                  95
Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala Thr
            100                 105                 110
Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met Glu
        115                 120                 125
Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys Glu
    130                 135                 140
Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly Ser
145                 150                 155                 160
Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro Arg
                165                 170                 175
Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln Thr
            180                 185                 190
Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr Gln
        195                 200                 205
Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala Ile
    210                 215                 220
Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala Glu
225                 230                 235                 240
Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr Val
                245                 250                 255
Met Ile Ala Lys Gly Phe Glu Leu Pro Trp Gly Pro Leu Ile Asn
            260                 265                 270 271
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INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1464 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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ATG TCT ATT TCA TCT TCT TCA GGA CCT GAC AAT CAA AAA AAT ATC ATG       48

Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile Met
 1               5                  10                  15

TCT CAA GTT CTG ACA TCG ACA CCC CAG GGC GTG CCC CAA CAA GAT AAG       96

Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp Lys
            20                  25                  30

CTG TCT GGC AAC GAA ACG AAG CAA ATA CAG CAA ACA CGT CAG GGT AAA      144

Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly Lys
        35                  40                  45

AAC ACT GAG ATG GAA AGC GAT GCC ACT ATT GCT GGT GCT TCT GGA AAA      192

Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly Lys
    50                  55                  60

GAC AAA ACT TCC TCG ACT ACA AAA ACA GAA ACA GCT CCA CAA CAG GGA      240

Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln Gly
65                  70                  75                  80

GTT GCT GCT GGG AAA GAA TCC TCA GAA AGT CAA AAG GCA GGT GCT GAT      288

Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala Asp
                85                  90                  95
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ACT GGA GTA TCA GGA GCG GCT GCT ACT ACA GCA TCA AAT ACT GCA ACA      336

Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala Thr
            100                 105                 110

AAA ATT GCT ATG CAG ACC TCT ATT GAA GAG GCG AGC AAA AGT ATG GAG      384

Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met Glu
        115                 120                 125

TCT ACC TTA GAG TCA CTT CAA AGC CTC AGT GCC GCG CAA ATG AAA GAA      432

Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys Glu
    130                 135                 140

GTC GAA GCG GTT GTT GTT GCT GCC CTC TCA GGG AAA AGT TCG GGT TCC      480

Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly Ser
145                 150                 155                 160

GCA AAA TTG GAA ACA CCT GAG CTC CCC AAG CCC GGG GTG ACA CCA AGA      528

Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro Arg
                165                 170                 175

TCA GAG GTT ATC GAA ATC GGA CTC GCG CTT GCT AAA GCA ATT CAG ACA      576

Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln Thr
            180                 185                 190

TTG GGA GAA GCC ACA AAA TCT GCC TTA TCT AAC TAT GCA AGT ACA CAA      624

Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr Gln
        195                 200                 205

GCA CAA GCA GAC CAA ACA AAT AAA CTA GGT CTA GAA AAG CAA GCG ATA      672
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Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala Ile
    210                 215                 220
AAA ATC GAT AAA GAA CGA GAA GAA TAC CAA GAG ATG AAG GCT GCC GAA      720

Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala Glu
225                 230                 235                 240
CAG AAG TCT AAA GAT CTC GAA GGA ACA ATG GAT ACT GTC AAT ACT GTG      768

Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr Val
                245                 250                 255
ATG ATC GCG GTT TCT GTT GCC ATT ACA GTT ATT TCT ATT GTT GCT GCT      816

Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile Val Ala Ala
            260                 265                 270
ATT TTT ACA TGC GGA GCT GGA CTC GCT GGA CTC GCT GCG GGA GCT GCT      864

Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala Gly Ala Ala
        275                 280                 285
GTA GGT GCA GCG GCA GCT GGA GGT GCA GCA GGA GCT GCT GCC GCA ACC      912

Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala Ala Ala Thr
    290                 295                 300
ACG GTA GCA ACA CAA ATT ACA GTT CAA GCT GTT GTC CAA GCG GTG AAA      960

Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln Ala Val Lys
305                 310                 315                 320
CAA GCT GTT ATC ACA GCT GTC AGA CAA GCG ATC ACC GCG GCT ATA AAA     1008
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Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala Ala Ile Lys
                325                 330                 335

GCG GCT GTC AAA TCT GGA ATA AAA GCA TTT ATC AAA ACT TTA GTC AAA     1056

Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr Leu Val Lys
            340                 345                 350

GCG ATT GCC AAA GCC ATT TCT AAA GGA ATC TCT AAG GTT TTC GCT AAG     1104

Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val Phe Ala Lys
        355                 360                 365

GGA ACT CAA ATG ATT GCG AAG AAC TTC CCC AAG CTC TCG AAA GTC ATC     1152

Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser Lys Val Ile
    370                 375                 380

TCG TCT CTT ACC AGT AAA TGG GTC ACG GTT GGG GTT GGG GTT GTA GTT     1200

Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly Val Val Val
385                 390                 395                 400

GCG GCG CCT GCT CTC GGT AAA GGG ATT ATG CAA ATG CAG CTC TCG GAG     1248

Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln Leu Ser Glu
                405                 410                 415

ATG CAA CAA AAC GTC GCT CAA TTT CAG AAA GAA GTC GGA AAA CTG CAG     1296

Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly Lys Leu Gln
            420                 425                 430

GCT GCG GCT GAT ATG ATT TCT ATG TTC ACT CAA TTT TGG CAA CAG GCA     1344

Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp Gln Gln Ala
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         435                 440                 445

AGT AAA ATT GCC TCA AAA CAA ACA GGC GAG TCT AAT GAA ATG ACT CAA     1392

Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu Met Thr Gln
    450                 455                 460

AAA GCT ACC AAG CTG GGC GCT CAA ATC CTT AAA GCG TAT GCC GCA ATC     1440

Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr Ala Ala Ile
465                 470                 475                 480

AGC GGA GCC ATC GCT GGC GCA GCA                                     1464

Ser Gly Ala Ile Ala Gly Ala Ala
                485         488
```

INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:813

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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ATG TCT ATT TCA TCT TCT TCA GGA CCT GAC AAT CAA AAA AAT ATC ATG       48

Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile Met
 1               5                  10                  15

TCT CAA GTT CTG ACA TCG ACA CCC CAG GGC GTG CCC CAA CAA GAT AAG       96

Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp Lys
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                  20                  25                  30

CTG TCT GGC AAC GAA ACG AAG CAA ATA CAG CAA ACA CGT CAG GGT AAA      144

Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly Lys
          35                  40                  45

AAC ACT GAG ATG GAA AGC GAT GCC ACT ATT GCT GGT GCT TCT GGA AAA      192

Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly Lys
     50                  55                  60

GAC AAA ACT TCC TCG ACT ACA AAA ACA GAA ACA GCT CCA CAA CAG GGA      240

Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln Gly
 65                  70                  75                  80

GTT GCT GCT GGG AAA GAA TCC TCA GAA AGT CAA AAG GCA GGT GCT GAT      288

Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala Asp
                 85                  90                  95

ACT GGA GTA TCA GGA GCG GCT GCT ACT ACA GCA TCA AAT ACT GCA ACA      336

Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala Thr
            100                 105                 110

AAA ATT GCT ATG CAG ACC TCT ATT GAA GAG GCG AGC AAA AGT ATG GAG      384

Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met Glu
        115                 120                 125

TCT ACC TTA GAG TCA CTT CAA AGC CTC AGT GCC GCG CAA ATG AAA GAA      432

Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys Glu
    130                 135                 140
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GTC GAA GCG GTT GTT GTT GCT GCC CTC TCA GGG AAA AGT TCG GGT TCC      480

Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly Ser
145                 150                 155                 160

GCA AAA TTG GAA ACA CCT GAG CTC CCC AAG CCC GGG GTG ACA CCA AGA      528

Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro Arg
                165                 170                 175

TCA GAG GTT ATC GAA ATC GGA CTC GCG CTT GCT AAA GCA ATT CAG ACA      576

Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln Thr
            180                 185                 190

TTG GGA GAA GCC ACA AAA TCT GCC TTA TCT AAC TAT GCA AGT ACA CAA      624

Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr Gln
        195                 200                 205

GCA CAA GCA GAC CAA ACA AAT AAA CTA GGT CTA GAA AAG CAA GCG ATA      672

Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala Ile
    210                 215                 220

AAA ATC GAT AAA GAA CGA GAA GAA TAC CAA GAG ATG AAG GCT GCC GAA      720

Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala Glu
225                 230                 235                 240

CAG AAG TCT AAA GAT CTC GAA GGA ACA ATG GAT ACT GTC AAT ACT GTG      768

Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr Val
                245                 250                 255

ATG ATC GCG AAG GGG TTC GAA TTG CCA TGG GGG CCC TTA ATT AAT          813
```

Met Ile Ala Lys Gly Phe Glu Leu Pro Trp Gly Pro Leu Ile Asn
260 265 270 271

INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:259 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile Met
1 5 10 15

Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp Lys
20 25 30

Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly Lys
35 40 45

Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly Lys
50 55 60

Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln Gly
65 70 75 80

Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala Asp
85 90 95

Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala Thr
100 105 110

Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met Glu
115 120 125

Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys Glu

130 135 140

Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly Ser

145 150 155 160

Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro Arg

165 170 175

Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln Thr

180 185 190

Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr Gln

195 200 205

Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala Ile

210 215 220

Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala Glu

225 230 235 240

Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr Val

245 250 255

Met Ile Ala

259

INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:571 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Pro Lys Gln Ala Glu Tyr Thr Trp Gly Ser Lys Lys Ile Leu Asp

1 5 10 15

Asn Ile Glu Cys Leu Thr Glu Asp Val Ala Glu Phe Lys Asp Leu Leu

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                20                  25                  30
Tyr Thr Ala His Arg Ile Thr Ser Ser Glu Glu Glu Ser Asp Asn Glu
        35                  40                  45
Ile Gln Pro Gly Ala Ile Leu Lys Gly Thr Val Val Asp Ile Asn Lys
    50                  55                  60
Asp Phe Val Val Val Asp Val Gly Leu Lys Ser Glu Gly Val Ile Pro
65                  70                  75                  80
Met Ser Glu Phe Ile Asp Ser Ser Glu Gly Leu Val Leu Gly Ala Glu
                85                  90                  95
Val Glu Val Tyr Leu Asp Gln Ala Glu Asp Glu Glu Gly Lys Val Val
            100                 105                 110
Leu Ser Arg Glu Lys Ala Thr Arg Gln Arg Gln Trp Glu Tyr Ile Leu
        115                 120                 125
Ala His Cys Glu Glu Gly Ser Ile Val Lys Gly Gln Ile Thr Arg Lys
    130                 135                 140
Val Lys Gly Gly Leu Ile Val Asp Ile Gly Met Glu Ala Phe Leu Pro
145                 150                 155                 160
Gly Ser Gln Ile Asp Asn Lys Lys Ile Lys Asn Leu Asp Asp Tyr Val
                165                 170                 175
Gly Lys Val Cys Glu Phe Lys Ile Leu Lys Ile Asn Val Glu Arg Arg
            180                 185                 190
Asn Ile Val Val Ser Arg Arg Glu Leu Leu Glu Ala Glu Arg Ile Ser
        195                 200                 205
Lys Lys Ala Glu Leu Ile Glu Gln Ile Ser Ile Gly Glu Tyr Arg Lys
    210                 215                 220
Gly Val Val Lys Asn Ile Thr Asp Phe Gly Val Phe Leu Asp Leu Asp
225                 230                 235                 240
Gly Ile Asp Gly Leu Leu His Ile Thr Asp Met Thr Trp Lys Arg Ile
                245                 250                 255
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Arg His Pro Ser Glu Met Val Glu Leu Asn Gln Glu Leu Glu Val Ile
            260                 265                 270
Ile Leu Ser Val Asp Lys Glu Lys Gly Arg Val Ala Leu Gly Leu Lys
        275                 280                 285
Gln Lys Glu His Asn Pro Trp Glu Asp Ile Glu Lys Lys Tyr Pro Pro
    290                 295                 300
Gly Lys Arg Val Leu Gly Lys Ile Val Lys Leu Leu Pro Tyr Gly Ala
305                 310                 315                 320
Phe Ile Glu Ile Glu Glu Gly Ile Glu Gly Leu Ile His Ile Ser Glu
                325                 330                 335
Met Ser Trp Val Lys Asn Ile Val Asp Pro Ser Glu Val Val Asn Lys
            340                 345                 350
Gly Asp Glu Val Glu Ala Ile Val Leu Ser Ile Gln Lys Asp Glu Gly
        355                 360                 365
Lys Ile Ser Leu Gly Leu Lys Gln Thr Glu Arg Asn Pro Trp Asp Asn
    370                 375                 380
Ile Glu Glu Lys Tyr Pro Ile Gly Leu His Val Asn Ala Glu Ile Lys
380                 385                 390                 395
Asn Leu Thr Asn Tyr Gly Ala Phe Val Glu Leu Glu Pro Gly Ile Glu
                400                 405                 410
Gly Leu Ile His Ile Ser Asp Met Ser Trp Ile Lys Lys Val Ser His
            415                 420                 425
Pro Ser Glu Leu Phe Lys Lys Gly Asn Ser Val Glu Ala Val Ile Leu
        430                 435                 440
Ser Val Asp Lys Glu Ser Lys Lys Ile Thr Leu Gly Val Lys Gln Leu
    445                 450                 455
Ser Ser Asn Pro Trp Asn Glu Ile Glu Ala Met Phe Pro Ala Gly Thr
460                 465                 470                 475
Val Ile Ser Gly Val Val Thr Lys Ile Thr Ala Phe Gly Ala Phe Val
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480 485 490

Glu Leu Gln Asn Gly Ile Glu Gly Leu Ile His Val Ser Glu Leu Ser

495 500 505

Asp Lys Pro Phe Ala Lys Ile Glu Asp Ile Ile Ser Ile Gly Glu Asn

510 515 520

Val Ser Ala Lys Val Ile Lys Leu Asp Pro Asp His Lys Lys Val Ser

525 530 535

Leu Ser Val Lys Glu Tyr Leu Ala Asp Asn Ala Tyr Asp Gln Asp Ser

540 545 550 560

Arg Thr Glu Leu Asp Phe Lys Asp Ser Gln Gly

565 570 571

INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:777 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGTCTATTT CATCTTCTTC AGGACCTGAC AATCAAAAAA ATATCATGTC TCAAGTTCTG 60

ACATCGACAC CCCAGGGCGT GCCCCAACAA GATAAGCTGT CTGGCAACGA AACGAAGCAA 120

ATACAGCAAA CACGTCAGGG TAAAAACACT GAGATGGAAA GCGATGCCAC TATTGCTGGT 180

GCTTCTGGAA AAGACAAAAC TTCCTCGACT ACAAAAACAG AAACAGCTCC ACAACAGGGA 240

GTTGCTGCTG GGAAAGAATC CTCAGAAAGT CAAAAGGCAG GTGCTGATAC TGGAGTATCA 300

GGAGCGGCTG CTACTACAGC ATCAAATACT GCAACAAAAA TTGCTATGCA GACCTCTATT 360

GAAGAGGCGA GCAAAAGTAT GGAGTCTACC TTAGAGTCAC TTCAAAGCCT CAGTGCCGCG 420

CAAATGAAAG AAGTCGAAGC GGTTGTTGTT GCTGCCCTCT CAGGGAAAAG TTCGGGTTCC 480

GCAAAATTGG AAACACCTGA GCTCCCCAAG CCCGGGGTGA CACCAAGATC AGAGGTTATC 540

GAAATCGGAC TCGCGCTTGC TAAAGCAATT CAGACATTGG GAGAAGCCAC AAAATCTGCC 600

TTATCTAACT ATGCAAGTAC ACAAGCACAA GCAGACCAAA CAAATAAACT AGGTCTAGAA 660

AAGCAAGCGA TAAAAATCGA TAAAGAACGA GAAGAATACC AAGAGATGAA GGCTGCCGAA 720

CAGAAGTCTA AAGATCTCGA AGGAACAATG GATACTGTCA ATACTGTGAT GATCGCG 777

INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ATGCCAAAAC AAGCTGAATA TACTTGGGGA TCTAAAAAAA TTCTGGACAA TATAGAATGC 60

CTCACAGAAG ACGTTGCCGA ATTTAAAGAT TTGCTTTATA CGGCACACAG AATTACTTCG 120

AGCGAAGAAG AATCTGATAA CGAAATACAG CCTGGCGCCA TCCTAAAAGG TACCGTAGTT 180

GATATTAATA AAGACTTTGT CGTAGTTGAT GTTGGTCTGA AGTCTGAGGG AGTGATCCCT 240

ATGTCAGAGT TCATAGACTC TTCAGAAGGT TTAGTGCTTG GAGCTGAAGT AGAAGTCTAT 300

CTCGACCAAG CCGAAGACGA AGAGGGCAAA GTTGTCCTTT CTAGAGAAAA AGCCACACGA 360

CAACGTCAAT GGGAATACAT CTTAGCTCAT TGTGAAGAAG GTTCTATTGT TAAAGGTCAA 420

ATTACACGTA AAGTCAAAGG CGGCCTTATT GTAGATATTG GAATGGAAGC CTTCCTACCT 480

GGATCACAAA TTGACAACAA GAAAATCAAA AATTTAGATG ATTATGTCGG AAAAGTTTGT 540

GAATTCAAAA TTTTAAAAAT TAACGTTGAA CGTCGCAATA TTGTTGTCTC AAGAAGAGAA 600

CTCTTAGAAG CTGAGAGAAT CTCTAAGAAA GCCGAACTTA TTGAACAAAT TTCTATCGGA 660

GAATACCGCA AAGGAGTTGT TAAAAACATT ACTGACTTTG GTGTATTCTT AGATCTCGAT 720

GGTATTGACG GTCTTCTCCA CATTACCGAT ATGACCTGGA AGCGCATACG ACATCCTTCC 780

GAAATGGTCG AATTGAATCA AGAGTTGGAA GTAATTATTT TAAGCGTAGA TAAAGAAAAA 840

GGACGAGTTG CTCTAGGTCT CAAACAAAAA GAGCATAATC CTTGGGAAGA TATTGAGAAG 900

AAATACCCTC CTGGAAAACG AGTTCTTGGT AAAATTGTGA AGCTTCTCCC CTACGGAGCT 960

TTCATTGAAA TTGAAGAGGG CATTGAAGGT CTAATTCACA TTTCTGAAAT GTCTTGGGTG 1020

AAAAATATTG TAGATCCTAG TGAAGTCGTA AATAAAGGCG ATGAAGTTGA AGCCATTGTT 1080

CTATCTATTC AGAAGGACGA AGGAAAAATT TCTCTAGGAT TAAAGCAAAC AGAACGTAAT 1140

CCTTGGGACA ATATCGAAGA AAAATATCCT ATAGGTCTCC ATGTCAATGC TGAAATCAAG 1200

AACTTAACCA ATTACGGTGC TTTCGTTGAA TTAGAACCAG GAATTGAGGG TCTGATTCAT 1260

ATTTCTGACA TGAGTTGGAT TAAAAAAGTC TCTCACCCTT CAGAACTATT CAAAAAAGGA 1320

AATTCTGTAG AGGCTGTTAT TTTATCAGTA GACAAAGAAA GTAAAAAAAT TACTTTAGGA 1380

GTTAAGCAAT TAAGTTCTAA TCCTTGGAAT GAAATTGAAG CTATGTTCCC TGCTGGCACA 1440

GTAATTTCAG GAGTTGTGAC TAAAATCACT GCATTTGGAG CCTTTGTTGA GCTACAAAAC 1500

GGGATTGAAG GATTGATTCA CGTTTCAGAA CTTTCTGACA AGCCCTTTGC AAAAATTGAA 1560

GATATTATCT CCATTGGAGA AAATGTTTCT GCAAAAGTAA TTAAGCTAGA TCCAGATCAT 1620

AAAAAAGTTT CTCTTTCTGT AAAAGAATAC TTAGCTGACA ATGCTTATGA TCAAGACTCT 1680

AGGACTGAAT TAGATTTCAA GGATTCTCAA GG 1712

INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1048 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Chlamydia pneumoniae

(B) STRAIN: YK-41

(vii) IMMEDIATE SOURCE:

(B) CLONE: 53-3S

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 236 to 1012

(C) IDENTIFICATION METHOD: P

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCAGTATCGG CGGAATTCGA ACCCCTTCGC GGCTCTTTCT GGAACTCTAG AATCTTTACA 60

TCTCGAAGAG TTAACTCAAG GATTATTCCC TTCTGCCCAA GAAGATGCCA ACTTCGCAAA 120

GGAGTTATCT TCAGTAGTAC ACGGATTAAA AAACCTAACC ACTGTAGTTA ATAAACAAAT 180

GGTTAAAGGC GCTGAGTAAA GCCCTTTGCA GAATCAAACC CCTTAGGATA CAAAC ATG 238

Met

1

TCT ATT TCA TCT TCT TCA GGA CCT GAC AAT CAA AAA AAT ATC ATG TCT 286

Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile Met Ser

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                5                  10                  15
CAA GTT CTG ACA TCG ACA CCC CAG GGC GTG CCC CAA CAA GAT AAG CTG     334

Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp Lys Leu
          20                  25                  30
TCT GGC AAC GAA ACG AAG CAA ATA CAG CAA ACA CGT CAG GGT AAA AAC     382

Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly Lys Asn
     35                  40                  45
ACT GAG ATG GAA AGC GAT GCC ACT ATT GCT GGT GCT TCT GGA AAA GAC     430

Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly Lys Asp
 50                  55                  60                  65
AAA ACT TCC TCG ACT ACA AAA ACA GAA ACA GCT CCA CAA CAG GGA GTT     478

Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln Gly Val
                    70                  75                  80
GCT GCT GGG AAA GAA TCC TCA GAA AGT CAA AAG GCA GGT GCT GAT ACT     526

Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala Asp Thr
               85                  90                  95
GGA GTA TCA GGA GCG GCT GCT ACT ACA GCA TCA AAT ACT GCA ACA AAA     574

Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala Thr Lys
          100                 105                 110
ATT GCT ATG CAG ACC TCT ATT GAA GAG GCG AGC AAA AGT ATG GAG TCT     622

Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met Glu Ser
     115                 120                 125
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ACC TTA GAG TCA CTT CAA AGC CTC AGT GCC GCG CAA ATG AAA GAA GTC      670

Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys Glu Val
130                 135                 140                 145

GAA GCG GTT GTT GTT GCT GCC CTC TCA GGG AAA AGT TCG GGT TCC GCA      718

Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly Ser Ala
                150                 155                 160

AAA TTG GAA ACA CCT GAG CTC CCC AAG CCC GGG GTG ACA CCA AGA TCA      766

Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro Arg Ser
            165                 170                 175

GAG GTT ATC GAA ATC GGA CTC GCG CTT GCT AAA GCA ATT CAG ACA TTG      814

Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln Thr Leu
        180                 185                 190

GGA GAA GCC ACA AAA TCT GCC TTA TCT AAC TAT GCA AGT ACA CAA GCA      862

Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr Gln Ala
    195                 200                 205

CAA GCA GAC CAA ACA AAT AAA CTA GGT CTA GAA AAG CAA GCG ATA AAA      910

Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala Ile Lys
210                 215                 220                 225

ATC GAT AAA GAA CGA GAA GAA TAC CAA GAG ATG AAG GCT GCC GAA CAG      958

Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala Glu Gln
                230                 235                 240

AAG TCT AAA GAT CTC GAA GGA ACA ATG GAT ACT GTC AAT ACT GTG ATG     1006
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Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr Val Met

245 250 255

ATC GCG AAGGGGTTCG AATTCCAGCT GAGCGCCGGT CGCTAC 1048

Ile Ala

259

INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:5702 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(ii) MOLECULE TYPE: Other nucleic acid; Plasmid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ATCGATGTTA ACAGATCTAA GCTTAACTAA CTAACTCCGG AAAAGGAGGA ACTTCCATGA 60

TCAGTCTGAT TGCGGCGTTA GCGGTAGATC GCGTTATCGG CATGGAAAAC GCCATGCCGT 120

GGAACCTGCC TGCCGATCTC GCCTGGTTTA AACGCAACAC CTTAAATAAA CCCGTGATTA 180

TGGGCCGCCA TACCTGGGAA TCAATCGGTC GTCCGTTGCC AGGACGCAAA AATATTATCC 240

TCAGCAGTCA ACCGGGTACG GACGATCGCG TAACGTGGGT GAAGTCGGTG GATGAAGCCA 300

TCGCGGCGTG TGGTGACGTA CCAGAAATCA TGGTGATTGG CGGCGGTCGC GTTTATGAAC 360

AGTTCTTGCC AAAAGCGCAA AAACTGTATC TGACGCATAT CGACGCAGAA GTGGAAGGCG 420

ACACCCATTT CCCGGATTAC GAGCCGGATG ACTGGGAATC GGTATTCAGC GAATTCCACG 480

ATGCTGATGC GCAGAACTCT CACAGCTATG AGTTCGAAAT TCTGGAGCGG CGGATCCAAT 540

TCGAACCCCT TCGCGGCTCT TTCTGGAACT CTAGAATCTT TACATCTCGA AGAGTTAACT 600

CAAGGATTAT TCCCTTCTGC CCAAGAAGAT GCCAACTTCG CAAAGGAGTT ATCTTCAGTA 660

GTACACGGAT TAAAAAACCT AACCACTGTA GTTAATAAAC AAATGGTTAA AGGCGCTGAG 720

TAAAGCCCTT TGCAGAATCA AACCCCTTAG GATACAAACA TGTCTATTTC ATCTTCTTCA 780

GGACCTGACA ATCAAAAAAA TATCATGTCT CAAGTTCTGA CATCGACACC CCAGGGCGTG 840

CCCCAACAAG ATAAGCTGTC TGGCAACGAA ACGAAGCAAA TACAGCAAAC ACGTCAGGGT 900

AAAAACACTG AGATGGAAAG CGATGCCACT ATTGCTGGTG CTTCTGGAAA AGACAAAACT 960

TCCTCGACTA CAAAAACAGA AACAGCTCCA CAACAGGGAG TTGCTGCTGG GAAAGAATCC 1020

TCAGAAAGTC AAAAGGCAGG TGCTGATACT GGAGTATCAG GAGCGGCTGC TACTACAGCA 1080

TCAAATACTG CAACAAAAAT TGCTATGCAG ACCTCTATTG AAGAGGCGAG CAAAAGTATG 1140

GAGTCTACCT TAGAGTCACT TCAAAGCCTC AGTGCCGCGC AAATGAAAGA AGTCGAAGCG 1200

GTTGTTGTTG CTGCCCTCTC AGGGAAAAGT TCGGGTTCCG CAAAATTGGA AACACCTGAG 1260

CTCCCCAAGC CCGGGGTGAC ACCAAGATCA GAGGTTATCG AAATCGGACT CGCGCTTGCT 1320

AAAGCAATTC AGACATTGGG AGAAGCCACA AAATCTGCCT TATCTAACTA TGCAAGTACA 1380

CAAGCACAAG CAGACCAAAC AAATAAACTA GGTCTAGAAA AGCAAGCGAT AAAAATCGAT 1440

AAAGAACGAG AAGAATACCA AGAGATGAAG GCTGCCGAAC AGAAGTCTAA AGATCTCGAA 1500

GGAACAATGG ATACTGTCAA TACTGTGATG ATCGCGAAGG GGTTCGAATT GCCATGGGGG 1560

CCCTTAATTA ATTAACTCGA GAGATCCAGA TCTAATCGAT GATCCTCTAC GCCGGACGCA 1620

TCGTGGCCGG CATCACCGGC GCCACAGGTG CGGTTGCTGG CGCCTATATC GCCGACATCA 1680

CCGATGGGGA AGATCGGGCT CGCCACTTCG GGCTCATGAG CGCTTGTTTC GGCGTGGGTA 1740

TGGTGGCAGG CCCGTGGCCG GGGGACTGTT GGGCGCCATC TCCTTGCATG CACCATTCCT 1800

TGCGGCGGCG GTGCTCAACG GCCTCAACCT ACTACTGGGC TGCTTCCTAA TGCAGGAGTC 1860

GCATAAGGGA GAGCGTCGAC CGATGCCCTT GAGAGCCTTC AACCCAGTCA GCTCCTTCCG 1920

GTGGGCGCGG GGCATGACTA TCGTCGCCGC ACTTATGACT GTCTTCTTTA TCATGCAACT 1980

CGTAGGACAG GTGCCGGCAG CGCTCTGGGT CATTTTCGGC GAGGACCGCT TTCGCTGGAG 2040

CGCGACGATG ATCGGCCTGT CGCTTGCGGT ATTCGGAATC TTGCACGCCC TCGCTCAAGC 2100

CTTCGTCACT GGTCCCGCCA CCAAACGTTT CGGCGAGAAG CAGGCCATTA TCGCCGGCAT 2160

GGCGGCCGAC GCGCTGGGCT ACGTCTTGCT GGCGTTCGCG ACGCGAGGCT GGATGGCCTT 2220

CCCCATTATG ATTCTTCTCG CTTCCGGCGG CATCGGGATG CCCGCGTTGC AGGCCATGCT 2280

GTCCAGGCAG GTAGATGACG ACCATCAGGG ACAGCTTCAA GGATCGCTCG CGGCTCTTAC 2340

CAGCCTAACT TCGATCACTG GACCGCTGAT CGTCACGGCG ATTTATGCCG CCTCGGCGAG 2400

CACATGGAAC GGGTTGGCAT GGATTGTAGG CGCCGCCCTA TACCTTGTCT GCCTCCCCGC 2460

GTTGCGTCGC GGTGCATGGA GCCGGGCCAC CTCGACCTGA ATGGAAGCCG GCGGCACCTC 2520

GCTAACGGAT TCACCACTCC AAGAATTGGA GCCAATCAAT TCTTGCGGAG AACTGTGAAT 2580

GCGCAAACCA ACCCTTGGCA GAACATATCC ATCGCGTCCG CCATCTCCAG CAGCCGCACG 2640

CGGCGCATCT CGGGCAGCGT TGGGTCCTGG CCACGGGTGC GCATGATCGT GCTCCTGTCG 2700

TTGAGGACCC GGCTAGGCTG GCGGGGTTGC CTTACTGGTT AGCAGAATGA ATCACCGATA 2760

CGCGAGCGAA CGTGAAGCGA CTGCTGCTGC AAAACGTCTG CGACCTGAGC AACAACATGA 2820

ATGGTCTTCG GTTTCCGTGT TTCGTAAAGT CTGGAAACGC GGAAGTCAGC GCCCTGCACC 2880

ATTATGTTCC GGATCTGCAT CGCAGGATGC TGCTGGCTAC CCTGTGGAAC ACCTACATCT 2940

GTATTAACGA AGCGCTGGCA TTGACCCTGA GTGATTTTTC TCTGGTCCCG CCGCATCCAT 3000

ACCGCCAGTT GTTTACCCTC ACAACGTTCC AGTAACCGGG CATGTTCATC ATCAGTAACC 3060

CGTATCGTGA GCATCCTCTC TCGTTTCATC GGTATCATTA CCCCCATGAA CAGAAATTC 3120

CCCCTTACAC GGAGGCATCA AGTGACCAAA CAGGAAAAAA CCGCCCTTAA CATGGCCCG 3180

CTTTATCAGA AGCCAGACAT TAACGCTTCT GGAGAAACTC AACGAGCTGG ACGCGGATG 3240

AACAGGCAGA CATCTGTGAA TCGCTTCACG ACCACGCTGA TGAGCTTTAC CGCAGCTGC 3300

CTCGCGCGTT TCGGTGATGA CGGTGAAAAC CTCTGACACA TGCAGCTCCC GGAGACGGT 3360

CACAGCTTGT CTGTAAGCGG ATGCCGGGAG CAGACAAGCC CGTCAGGGCG CGTCAGCGG 3420

GTGTTGGCGG GTGTCGGGGC GCAGCCATGA CCCAGTCACG TAGCGATAGC GGAGTGTAT 3480

ACTGGCTTAA CTATGCGGCA TCAGAGCAGA TTGTACTGAG AGTGCACCAT ATGCGGTGT 3540

GAAATACCGC ACAGATGCGT AAGGAGAAAA TACCGCATCA GGCGCTCTTC CGCTTCCTC 3600

GCTCACTGAC TCGCTGCGCT CGGTCGTTCG GCTGCGGCGA GCGGTATCAG CTCACTCAA 3660

AGGCGGTAAT ACGGTTATCC ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCA 3720

AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCGCGT TGCTGGCGTT TTTCCATAG 3780

GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA AGTCAGAGGT GGCGAAACC 3840

CGACAGGACT ATAAAGATAC CAGGCGTTTC CCCCTGGAAG CTCCCTCGTG CGCTCTCCT 3900

GTTCCGACCC TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGC 3960

GCTTTCTCAA TGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGGTCGTTC GCTCCAAGC 4020

TGGGCTGTGT GCACGAACCC CCCGTTCAGC CCGACCGCTG CGCCTTATCC GGTAACTAT 4080

CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC CACTGGTAA 4140

CAGGATTAGC AGAGCGAGGT ATGTAGGCGG TGCTACAGAG TTCTTGAAGT GGTGGCCTA 4200

ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC TCTGCTGAAG CCAGTTACC 4260

TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA CCACCGCTGG TAGCGGTGG 4320

TTTTTTTGTT TGCAAGCAGC AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCTT 4380

TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA GGGATTTTG 4440

GTCATGAGAT TATCAAAAAG GATCTTCACC TAGATCCTTT TAAATTAAAA ATGAAGTTT 4500

TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAT GCTTAATCA 4560

GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTCATC CATAGTTGCC TGACTCCCC 4620

GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG GCCCCAGTGC TGCAATGAT 4680

ACCGCGAGAC CCACGCTCAC CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAA 4740

GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAATTGT 4800

TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT TGTTGCCAT 4860

TGCTGCAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTT 4920

CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG CAAAAAAGCG GTTAGCTCC 4980

TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAG TGTTATCACT CATGGTTAT 5040

GGCAGCACTG CATAATTCTC TTACTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTG 5100

GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCGAGT TGCTCTTGC 5160

CCGGCGTCAA CACGGGATAA TACCGCGCCA CATAGCAGAA CTTTAAAAGT GCTCATCAT 5220

TGGAAAACGT TCTTCGGGGC GAAAACTCTC AAGGATCTTA CCGCTGTTGA GATCCAGTT 5280

CGATGTAACC CACTCGTGCA CCCAACTGAT CTTCAGCATC TTTTACTTTC ACCAGCGTT 5340

TCTGGGTGAG CAAAAACAGG AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACG 5400

GAAATGTTGA ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTT 5460

ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTT 5520

CCGCGCACAT TTCCCCGAAA AGTGCCACCT GACGTCTAAG AAACCATTAT TATCATGAC 5580

ATTAACCTAT AAAAATAGGC GTATCACGAG GCCCTTTCGT CTTCAAGAAT TAATTGTTA 5640

TCCGCTCACA ATTAATTCTT GACAATTAGT TAACTATTTG TTATAATGTA TTCATAAGC 5700

TT 5702

INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GATCCAATTG CCATGGGGGC CCTTAATTAA TTAAC 35

INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TCGAGTTAAT TAATTAAGGG CCCCCATGGC AATTG 35

INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1954 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Chlamydia pneumoniae

(B) STRAIN: YK-41

(vii) IMMEDIATE SOURCE:

(B) CLONE: 70-2S

(ix) FEATURE:

(A) NAME/KEY: -35 signal

(B) LOCATION:146 to 151

(C) IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus sequence

(ix) FEATURE:

(A) NAME/KEY: -10 signal

(B) LOCATION:169 to 174

(C) IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus sequence

(ix) FEATURE:

(A) NAME/KEY: RBS

(B) LOCATION:199 to 205

(C) IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus sequence

(ix) FEATURE:

(A) NAME/KEY:CDS

(B) LOCATION:215 to 1927

(C) IDENTIFICATION METHOD: by similarity with known sequence or to an established consensus sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

```
TTGACACCAG ACCAACTGGT AATGGTAGCG ACCGGCGCTC AGCTGGAATT CGAACCCCTT      60

CGCCTTATAC ATCTCTAGAA CGGAAGTATA GGATTTTACG ATTAATTCGA TTATATAGAA     120

CTAATCGTCT CCTGCAAGGG AGGTCTTGCC TTTTTTAAGG TTTATATTTA CACTGTCTTT     180

TTTGACTTTG TAGTTTTTAG GAGAATAACA ATAA ATG CCA AAA CAA GCT GAA TAT     235
                                      Met Pro Lys Gln Ala Glu Tyr
                                        1               5

ACT TGG GGA TCT AAA AAA ATT CTG GAC AAT ATA GAA TGC CTC ACA GAA       283
Thr Trp Gly Ser Lys Lys Ile Leu Asp Asn Ile Glu Cys Leu Thr Glu
          10                  15                  20

GAC GTT GCC GAA TTT AAA GAT TTG CTT TAT ACG GCA CAC AGA ATT ACT       331
Asp Val Ala Glu Phe Lys Asp Leu Leu Tyr Thr Ala His Arg Ile Thr
     25                  30                  35

TCG AGC GAA GAA GAA TCT GAT AAC GAA ATA CAG CCT GGC GCC ATC CTA       379
Ser Ser Glu Glu Glu Ser Asp Asn Glu Ile Gln Pro Gly Ala Ile Leu
 40                  45                  50                  55

AAA GGT ACC GTA GTT GAT ATT AAT AAA GAC TTT GTC GTA GTT GAT GTT       427
Lys Gly Thr Val Val Asp Ile Asn Lys Asp Phe Val Val Val Asp Val
```

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                    60                  65                  70
GGT CTG AAG TCT GAG GGA GTG ATC CCT ATG TCA GAG TTC ATA GAC TCT      475

Gly Leu Lys Ser Glu Gly Val Ile Pro Met Ser Glu Phe Ile Asp Ser
                75                  80                  85
TCA GAA GGT TTA GTG CTT GGA GCT GAA GTA GAA GTC TAT CTC GAC CAA      523

Ser Glu Gly Leu Val Leu Gly Ala Glu Val Glu Val Tyr Leu Asp Gln
          90                  95                 100
GCC GAA GAC GAA GAG GGC AAA GTT GTC CTT TCT AGA GAA AAA GCC ACA      571

Ala Glu Asp Glu Glu Gly Lys Val Val Leu Ser Arg Glu Lys Ala Thr
    105                 110                 115
CGA CAA CGT CAA TGG GAA TAC ATC TTA GCT CAT TGT GAA GAA GGT TCT      619

Arg Gln Arg Gln Trp Glu Tyr Ile Leu Ala His Cys Glu Glu Gly Ser
120                 125                 130                 135
ATT GTT AAA GGT CAA ATT ACA CGT AAA GTC AAA GGC GGC CTT ATT GTA      667

Ile Val Lys Gly Gln Ile Thr Arg Lys Val Lys Gly Gly Leu Ile Val
                140                 145                 150
GAT Ile Gly Met Glu Ala Phe Leu Pro Gly Ser Gln Ile Asp Asn Lys      715

Asp ATT GGA ATG GAA GCC TTC CTA CCT GGA TCA CAA ATT GAC AAC AAG
            155                 160                 165
Lys ATC AAA AAT TTA GAT GAT TAT GTC GGA AAA GTT TGT GAA TTC AAA      763

AAA Ile Lys Asn Leu Asp Asp Tyr Val Gly Lys Val Cys Glu Phe Lys
        170                 175                 180
```

```
ATT TTA AAA ATT AAC GTT GAA CGT CGC AAT ATT GTT GTC TCA AGA AGA      811

Ile Leu Lys Ile Asn Val Glu Arg Arg Asn Ile Val Val Ser Arg Arg
    185                 190                 195
GAA CTC TTA GAA GCT GAG AGA ATC TCT AAG AAA GCC GAA CTT ATT GAA      859

Glu Leu Leu Glu Ala Glu Arg Ile Ser Lys Lys Ala Glu Leu Ile Glu
200                 205                 210                 215
CAA ATT TCT ATC GGA GAA TAC CGC AAA GGA GTT GTT AAA AAC ATT ACT      907

Gln Ile Ser Ile Gly Glu Tyr Arg Lys Gly Val Val Lys Asn Ile Thr
                220                 225                 230
GAC TTT GGT GTA TTC TTA GAT CTC GAT GGT ATT GAC GGT CTT CTC CAC      955

Asp Phe Gly Val Phe Leu Asp Leu Asp Gly Ile Asp Gly Leu Leu His
            235                 240                 245
ATT ACC GAT ATG ACC TGG AAG CGC ATA CGA CAT CCT TCC GAA ATG GTC     1003

Ile Thr Asp Met Thr Trp Lys Arg Ile Arg His Pro Ser Glu Met Val
        250                 255                 260
GAA TTG AAT CAA GAG TTG GAA GTA ATT ATT TTA AGC GTA GAT AAA GAA     1051

Glu Leu Asn Gln Glu Leu Glu Val Ile Ile Leu Ser Val Asp Lys Glu
    265                 270                 275
AAA GGA CGA GTT GCT CTA GGT CTC AAA CAA AAA GAG CAT AAT CCT TGG     1099

Lys Gly Arg Val Ala Leu Gly Leu Lys Gln Lys Glu His Asn Pro Trp
280                 285                 290                 295
GAA GAT ATT GAG AAG AAA TAC CCT CCT GGA AAA CGA GTT CTT GGT AAA     1147
```

```
Glu Asp Ile Glu Lys Lys Tyr Pro Pro Gly Lys Arg Val Leu Gly Lys
                300                 305                 310

ATT GTG AAG CTT CTC CCC TAC GGA GCT TTC ATT GAA ATT GAA GAG GGC    1195

Ile Val Lys Leu Leu Pro Tyr Gly Ala Phe Ile Glu Ile Glu Glu Gly
            315                 320                 325

ATT GAA GGT CTA ATT CAC ATT TCT GAA ATG TCT TGG GTG AAA AAT ATT    1243

Ile Glu Gly Leu Ile His Ile Ser Glu Met Ser Trp Val Lys Asn Ile
        330                 335                 340

GTA GAT CCT AGT GAA GTC GTA AAT AAA GGC GAT GAA GTT GAA GCC ATT    1291

Val Asp Pro Ser Glu Val Val Asn Lys Gly Asp Glu Val Glu Ala Ile
    345                 350                 355

GTT CTA TCT ATT CAG AAG GAC GAA GGA AAA ATT TCT CTA GGA TTA AAG    1339

Val Leu Ser Ile Gln Lys Asp Glu Gly Lys Ile Ser Leu Gly Leu Lys
360                 365                 370                 375

CAA ACA GAA CGT AAT CCT TGG GAC AAT ATC GAA GAA AAA TAT CCT ATA    1387

Gln Thr Glu Arg Asn Pro Trp Asp Asn Ile Glu Glu Lys Tyr Pro Ile
                380                 385                 390

GGT CTC CAT GTC AAT GCT GAA ATC AAG AAC TTA ACC AAT TAC GGT GCT    1435

Gly Leu His Val Asn Ala Glu Ile Lys Asn Leu Thr Asn Tyr Gly Ala
            395                 400                 405

TTC GTT GAA TTA GAA CCA GGA ATT GAG GGT CTG ATT CAT ATT TCT GAC    1483
```

```
Phe Val Glu Leu Glu Pro Gly Ile Glu Gly Leu Ile His Ile Ser Asp
        410                 415                 420
ATG AGT TGG ATT AAA AAA GTC TCT CAC CCT TCA GAA CTA TTC AAA AAA    1531

Met Ser Trp Ile Lys Lys Val Ser His Pro Ser Glu Leu Phe Lys Lys
    425                 430                 435
GGA AAT TCT GTA GAG GCT GTT ATT TTA TCA GTA GAC AAA GAA AGT AAA    1579

Gly Asn Ser Val Glu Ala Val Ile Leu Ser Val Asp Lys Glu Ser Lys
440                 445                 450                 455
AAA ATT ACT TTA GGA GTT AAG CAA TTA AGT TCT AAT CCT TGG AAT GAA    1627

Lys Ile Thr Leu Gly Val Lys Gln Leu Ser Ser Asn Pro Trp Asn Glu
                460                 465                 470
ATT GAA GCT ATG TTC CCT GCT GGC ACA GTA ATT TCA GGA GTT GTG ACT    1675

Ile Glu Ala Met Phe Pro Ala Gly Thr Val Ile Ser Gly Val Val Thr
            475                 480                 485
AAA ATC ACT GCA TTT GGA GCC TTT GTT GAG CTA CAA AAC GGG ATT GAA    1723

Lys Ile Thr Ala Phe Gly Ala Phe Val Glu Leu Gln Asn Gly Ile Glu
        490                 495                 500
GGA TTG ATT CAC GTT TCA GAA CTT TCT GAC AAG CCC TTT GCA AAA ATT    1771

Gly Leu Ile His Val Ser Glu Leu Ser Asp Lys Pro Phe Ala Lys Ile
    505                 510                 515
GAA GAT ATT ATC TCC ATT GGA GAA AAT GTT TCT GCA AAA GTA ATT AAG    1919

Glu Asp Ile Ile Ser Ile Gly Glu Asn Val Ser Ala Lys Val Ile Lys
```

```
520                 525                 530                 535

CTA GAT CCA GAT CAT AAA AAA GTT TCT CTT TCT GTA AAA GAA TAC TTA     1867

Leu Asp Pro Asp His Lys Lys Val Ser Leu Ser Val Lys Glu Tyr Leu

                540                 545                 550

GCT GAC AAT GCT TAT GAT CAA GAC TCT AGG ACT GAA TTA GAT TTC AAG     1915

Ala Asp Asn Ala Tyr Asp Gln Asp Ser Arg Thr Glu Leu Asp Phe Lys

            555                 560                 565

GAT TCT CAA GGC GAA GGG GTT CGA ATT CCG CCG ATA CTG                 1954

Asp Ser Gln Gly Glu Gly Val Arg Ile Pro Pro Ile Leu

        570                 575                 580
```

INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:160 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
Met Ile Ser Leu Ile Ala Ala Leu Ala Val Asp Arg Val Ile Gly Met
  1               5                  10                  15

Glu Asn Ala Met Pro Trp Asn Leu Pro Ala Asp Leu Ala Trp Phe Lys

            20                  25                  30

Arg Asn Thr Leu Asn Lys Pro Val Ile Met Gly Arg His Thr Trp Glu

        35                  40                  45

Ser Ile Gly Arg Pro Leu Pro Gly Arg Lys Asn Ile Ile Leu Ser Ser

    50                  55                  60
```

```
Gln Pro Gly Thr Asp Asp Arg Val Thr Trp Val Lys Ser Val Asp Glu
 65                  70                  75                  80
Ala Ile Ala Ala Cys Gly Asp Val Pro Glu Ile Met Val Ile Gly Gly
                 85                  90                  95
Gly Arg Val Tyr Glu Gln Phe Leu Pro Lys Ala Gln Lys Leu Tyr Leu
            100                 105                 110
Thr His Ile Asp Ala Glu Val Glu Gly Asp Thr His Phe Pro Asp Tyr
        115                 120                 125
Glu Pro Asp Asp Trp Glu Ser Val Phe Ser Glu Phe His Asp Ala Asp
    130                 135                 140
Ala Gln Asn Ser His Ser Tyr Glu Phe Glu Ile Leu Glu Arg Arg Ile
145                 150                 155                 160
```

INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:649 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```
Met Ile Ser Leu Ile Ala Ala Leu Ala Val Asp Arg Val Ile Gly Met
  1               5                  10                  15
Glu Asn Ala Met Pro Trp Asn Leu Pro Ala Asp Leu Ala Trp Phe Lys
             20                  25                  30
Arg Asn Thr Leu Asn Lys Pro Val Ile Met Gly Arg His Thr Trp Glu
         35                  40                  45
Ser Ile Gly Arg Pro Leu Pro Gly Arg Lys Asn Ile Ile Leu Ser Ser
     50                  55                  60
Gln Pro Gly Thr Asp Asp Arg Val Thr Trp Val Lys Ser Val Asp Glu
```

65 70 75 80

Ala Ile Ala Ala Cys Gly Asp Val Pro Glu Ile Met Val Ile Gly Gly

85 90 95

Gly Arg Val Tyr Glu Gln Phe Leu Pro Lys Ala Gln Lys Leu Tyr Leu

100 105 110

Thr His Ile Asp Ala Glu Val Glu Gly Asp Thr His Phe Pro Asp Tyr

115 120 125

Glu Pro Asp Asp Trp Glu Ser Val Phe Ser Glu Phe His Asp Ala Asp

130 135 140

Ala Gln Asn Ser His Ser Tyr Glu Phe Glu Ile Leu Glu Arg Arg Ile

145 150 155 160

Leu Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile

165 170 175

Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp

180 185 190

Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly

195 200 205

Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly

210 215 220

Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln

225 230 235 240

Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala

245 250 255

Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala

260 265 270

Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met

275 280 285

Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys

290 295 300

Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly
305 310 315 320
Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro
325 330 335
Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln
340 345 350
Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr
355 360 365
Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala
370 375 380
Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala
385 390 395 400
Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr
405 410 415
Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile Val Ala
420 425 430
Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala Gly Ala
435 440 445
Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala Ala Ala
450 455 460
Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln Ala Val
465 470 475 480
Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala Ala Ile
485 490 495
Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr Leu Val
500 505 510
Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val Phe Ala
515 520 525
Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser Lys Val

530 535 540

Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly Val Val

545 550 555 560

Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln Leu Ser

565 570 575

Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly Lys Leu

580 585 590

Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp Gln Gln

595 600 605

Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu Met Thr

610 615 620

Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr Ala Ala

625 630 635 640

Ile Ser Gly Ala Ile Ala Gly Ala Ala

645 649

INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:432 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Ile Ser Leu Ile Ala Ala Leu Ala Val Asp Arg Val Ile Gly Met

1 5 10 15

Glu Asn Ala Met Pro Trp Asn Leu Pro Ala Asp Leu Ala Trp Phe Lys

20 25 30

Arg Asn Thr Leu Asn Lys Pro Val Ile Met Gly Arg His Thr Trp Glu

35 40 45

```
Ser Ile Gly Arg Pro Leu Pro Gly Arg Lys Asn Ile Ile Leu Ser Ser
     50                  55                  60
Gln Pro Gly Thr Asp Asp Arg Val Thr Trp Val Lys Ser Val Asp Glu
 65                  70                  75                  80
Ala Ile Ala Ala Cys Gly Asp Val Pro Glu Ile Met Val Ile Gly Gly
                 85                  90                  95
Gly Arg Val Tyr Glu Gln Phe Leu Pro Lys Ala Gln Lys Leu Tyr Leu
            100                 105                 110
Thr His Ile Asp Ala Glu Val Glu Gly Asp Thr His Phe Pro Asp Tyr
        115                 120                 125
Glu Pro Asp Asp Trp Glu Ser Val Phe Ser Glu Phe His Asp Ala Asp
    130                 135                 140
Ala Gln Asn Ser His Ser Tyr Glu Phe Glu Ile Leu Glu Arg Arg Ile
145                 150                 155                 160
Leu Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile
                165                 170                 175
Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp
            180                 185                 190
Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly
        195                 200                 205
Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly
    210                 215                 220
Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln
225                 230                 235                 240
Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala
                245                 250                 255
Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala
            260                 265                 270
Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met
```

275 280 285

Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys

290 295 300

Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly

305 310 315 320

Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro

325 330 335

Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln

340 345 350

Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr

355 360 365

Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala

370 375 380

Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala

385 390 395 400

Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr

405 410 415

Val Met Ile Ala Lys Gly Phe Glu Leu Pro Trp Gly Pro Leu Ile Asn

420 425 430 432

INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1947 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATG ATC AGT CTG ATT GCG GCG TTA GCG GTA GAT CGC GTT ATC GGC ATG 48

```
Met Ile Ser Leu Ile Ala Ala Leu Ala Val Asp Arg Val Ile Gly Met
 1               5                  10                  15
GAA AAC GCC ATG CCG TGG AAC CTG CCT GCC GAT CTC GCC TGG TTT AAA      96

Glu Asn Ala Met Pro Trp Asn Leu Pro Ala Asp Leu Ala Trp Phe Lys
            20                  25                  30
CGC AAC ACC TTA AAT AAA CCC GTG ATT ATG GGC CGC CAT ACC TGG GAA     144

Arg Asn Thr Leu Asn Lys Pro Val Ile Met Gly Arg His Thr Trp Glu
        35                  40                  45
TCA ATC GGT CGT CCG TTG CCA GGA CGC AAA AAT ATT ATC CTC AGC AGT     192

Ser Ile Gly Arg Pro Leu Pro Gly Arg Lys Asn Ile Ile Leu Ser Ser
    50                  55                  60
CAA CCG GGT ACG GAC GAT CGC GTA ACG TGG GTG AAG TCG GTG GAT GAA     240

Gln Pro Gly Thr Asp Asp Arg Val Thr Trp Val Lys Ser Val Asp Glu
65                  70                  75                  80
GCC ATC GCG GCG TGT GGT GAC GTA CCA GAA ATC ATG GTG ATT GGC GGC     288

Ala Ile Ala Ala Cys Gly Asp Val Pro Glu Ile Met Val Ile Gly Gly
                85                  90                  95
GGT CGC GTT TAT GAA CAG TTC TTG CCA AAA GCG CAA AAA CTG TAT CTG     336

Gly Arg Val Tyr Glu Gln Phe Leu Pro Lys Ala Gln Lys Leu Tyr Leu
            100                 105                 110
ACG CAT ATC GAC GCA GAA GTG GAA GGC GAC ACC CAT TTC CCG GAT TAC     384
```

```
Thr His Ile Asp Ala Glu Val Glu Gly Asp Thr His Phe Pro Asp Tyr
        115                 120                 125
GAG CCG GAT GAC TGG GAA TCG GTA TTC AGC GAA TTC CAC GAT GCT GAT      432

Glu Pro Asp Asp Trp Glu Ser Val Phe Ser Glu Phe His Asp Ala Asp
    130                 135                 140
GCG CAG AAC TCT CAC AGC TAT GAG TTC GAA ATT CTG GAG CGG CGG ATC      480

Ala Gln Asn Ser His Ser Tyr Glu Phe Glu Ile Leu Glu Arg Arg Ile
145                 150                 155                 160
CTG ATG TCT ATT TCA TCT TCT TCA GGA CCT GAC AAT CAA AAA AAT ATC      528

Leu Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile
                165                 170                 175
ATG TCT CAA GTT CTG ACA TCG ACA CCC CAG GGC GTG CCC CAA CAA GAT      576

Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp
            180                 185                 190
AAG CTG TCT GGC AAC GAA ACG AAG CAA ATA CAG CAA ACA CGT CAG GGT      624

Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly
        195                 200                 205
AAA AAC ACT GAG ATG GAA AGC GAT GCC ACT ATT GCT GGT GCT TCT GGA      672

Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly
    210                 215                 220
AAA GAC AAA ACT TCC TCG ACT ACA AAA ACA GAA ACA GCT CCA CAA CAG      720

Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln
```

```
225                 230                 235                 240
GGA GTT GCT GCT GGG AAA GAA TCC TCA GAA AGT CAA AAG GCA GGT GCT      768

Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala
                245                 250                 255
GAT ACT GGA GTA TCA GGA GCG GCT GCT ACT ACA GCA TCA AAT ACT GCA      816

Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala
            260                 265                 270
ACA AAA ATT GCT ATG CAG ACC TCT ATT GAA GAG GCG AGC AAA AGT ATG      864

Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met
        275                 280                 285
GAG TCT ACC TTA GAG TCA CTT CAA AGC CTC AGT GCC GCG CAA ATG AAA      912

Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys
    290                 295                 300
GAA GTC GAA GCG GTT GTT GTT GCT GCC CTC TCA GGG AAA AGT TCG GGT      960

Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly
305                 310                 315                 320
TCC GCA AAA TTG GAA ACA CCT GAG CTC CCC AAG CCC GGG GTG ACA CCA     1008

Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro
                325                 330                 335
AGA TCA GAG GTT ATC GAA ATC GGA CTC GCG CTT GCT AAA GCA ATT CAG     1056

Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln
            340                 345                 350
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ACA TTG GGA GAA GCC ACA AAA TCT GCC TTA TCT AAC TAT GCA AGT ACA      1104

Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr
        355                 360                 365

CAA GCA CAA GCA GAC CAA ACA AAT AAA CTA GGT CTA GAA AAG CAA GCG      1152

Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala
    370                 375                 380

ATA AAA ATC GAT AAA GAA CGA GAA GAA TAC CAA GAG ATG AAG GCT GCC      1200

Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala
385                 390                 395                 400

GAA CAG AAG TCT AAA GAT CTC GAA GGA ACA ATG GAT ACT GTC AAT ACT      1248

Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr
                405                 410                 415

GTG ATG ATC GCG GTT TCT GTT GCC ATT ACA GTT ATT TCT ATT GTT GCT      1296

Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile Val Ala
            420                 425                 430

GCT ATT TTT ACA TGC GGA GCT GGA CTC GCT GGA CTC GCT GCG GGA GCT      1344

Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala Gly Ala
        435                 440                 445

GCT GTA GGT GCA GCG GCA GCT GGA GGT GCA GCA GGA GCT GCT GCC GCA      1392

Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala Ala Ala
    450                 455                 460

ACC ACG GTA GCA ACA CAA ATT ACA GTT CAA GCT GTT GTC CAA GCG GTG      1440
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Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln Ala Val
465                 470                 475                 480
AAA CAA GCT GTT ATC ACA GCT GTC AGA CAA GCG ATC ACC GCG GCT ATA     1488

Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala Ala Ile
                485                 490                 495
AAA GCG GCT GTC AAA TCT GGA ATA AAA GCA TTT ATC AAA ACT TTA GTC     1536

Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr Leu Val
            500                 505                 510
AAA GCG ATT GCC AAA GCC ATT TCT AAA GGA ATC TCT AAG GTT TTC GCT     1584

Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val Phe Ala
        515                 520                 525
AAG GGA ACT CAA ATG ATT GCG AAG AAC TTC CCC AAG CTC TCG AAA GTC     1632

Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser Lys Val
    530                 535                 540
ATC TCG TCT CTT ACC AGT AAA TGG GTC ACG GTT GGG GTT GGG GTT GTA     1680

Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly Val Val
545                 550                 555                 560
GTT GCG GCG CCT GCT CTC GGT AAA GGG ATT ATG CAA ATG CAG CTC TCG     1728

Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln Leu Ser
                565                 570                 575
GAG ATG CAA CAA AAC GTC GCT CAA TTT CAG AAA GAA GTC GGA AAA CTG     1776
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Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly Lys Leu
            580                 585                 590

CAG GCT GCG GCT GAT ATG ATT TCT ATG TTC ACT CAA TTT TGG CAA CAG    1824

Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp Gln Gln
        595                 600                 605

GCA AGT AAA ATT GCC TCA AAA CAA ACA GGC GAG TCT AAT GAA ATG ACT    1872

Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu Met Thr
    610                 615                 620

CAA AAA GCT ACC AAG CTG GGC GCT CAA ATC CTT AAA GCG TAT GCC GCA    1920

Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr Ala Ala
625                 630                 635                 640

ATC AGC GGA GCC ATC GCT GGC GCA GCA                               1947

Ile Ser Gly Ala Ile Ala Gly Ala Ala
                645             649
```

INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1296 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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ATG ATC AGT CTG ATT GCG GCG TTA GCG GTA GAT CGC GTT ATC GGC ATG      48
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Met Ile Ser Leu Ile Ala Ala Leu Ala Val Asp Arg Val Ile Gly Met
  1               5                  10                  15
GAA AAC GCC ATG CCG TGG AAC CTG CCT GCC GAT CTC GCC TGG TTT AAA      96

Glu Asn Ala Met Pro Trp Asn Leu Pro Ala Asp Leu Ala Trp Phe Lys
             20                  25                  30
CGC AAC ACC TTA AAT AAA CCC GTG ATT ATG GGC CGC CAT ACC TGG GAA     144

Arg Asn Thr Leu Asn Lys Pro Val Ile Met Gly Arg His Thr Trp Glu
         35                  40                  45
TCA ATC GGT CGT CCG TTG CCA GGA CGC AAA AAT ATT ATC CTC AGC AGT     192

Ser Ile Gly Arg Pro Leu Pro Gly Arg Lys Asn Ile Ile Leu Ser Ser
     50                  55                  60
CAA CCG GGT ACG GAC GAT CGC GTA ACG TGG GTG AAG TCG GTG GAT GAA     240

Gln Pro Gly Thr Asp Asp Arg Val Thr Trp Val Lys Ser Val Asp Glu
 65                  70                  75                  80
GCC ATC GCG GCG TGT GGT GAC GTA CCA GAA ATC ATG GTG ATT GGC GGC     288

Ala Ile Ala Ala Cys Gly Asp Val Pro Glu Ile Met Val Ile Gly Gly
                 85                  90                  95
GGT CGC GTT TAT GAA CAG TTC TTG CCA AAA GCG CAA AAA CTG TAT CTG     336

Gly Arg Val Tyr Glu Gln Phe Leu Pro Lys Ala Gln Lys Leu Tyr Leu
            100                 105                 110
ACG CAT ATC GAC GCA GAA GTG GAA GGC GAC ACC CAT TTC CCG GAT TAC     384

Thr His Ile Asp Ala Glu Val Glu Gly Asp Thr His Phe Pro Asp Tyr
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         115                 120                 125
GAG CCG GAT GAC TGG GAA TCG GTA TTC AGC GAA TTC CAC GAT GCT GAT      432

Glu Pro Asp Asp Trp Glu Ser Val Phe Ser Glu Phe His Asp Ala Asp
    130                 135                 140
GCG CAG AAC TCT CAC AGC TAT GAG TTC GAA ATT CTG GAG CGG CGG ATC      480

Ala Gln Asn Ser His Ser Tyr Glu Phe Glu Ile Leu Glu Arg Arg Ile
145                 150                 155                 160
CTG ATG TCT ATT TCA TCT TCT TCA GGA CCT GAC AAT CAA AAA AAT ATC      528

Leu Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile
                165                 170                 175
ATG TCT CAA GTT CTG ACA TCG ACA CCC CAG GGC GTG CCC CAA CAA GAT      576

Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp
            180                 185                 190
AAG CTG TCT GGC AAC GAA ACG AAG CAA ATA CAG CAA ACA CGT CAG GGT      624

Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly
        195                 200                 205
AAA AAC ACT GAG ATG GAA AGC GAT GCC ACT ATT GCT GGT GCT TCT GGA      672

Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly
    210                 215                 220
AAA GAC AAA ACT TCC TCG ACT ACA AAA ACA GAA ACA GCT CCA CAA CAG      720

Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln
225                 230                 235                 240
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GGA GTT GCT GCT GGG AAA GAA TCC TCA GAA AGT CAA AAG GCA GGT GCT      768

Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala
                245                 250                 255

GAT ACT GGA GTA TCA GGA GCG GCT GCT ACT ACA GCA TCA AAT ACT GCA      816

Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala
            260                 265                 270

ACA AAA ATT GCT ATG CAG ACC TCT ATT GAA GAG GCG AGC AAA AGT ATG      864

Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met
        275                 280                 285

GAG TCT ACC TTA GAG TCA CTT CAA AGC CTC AGT GCC GCG CAA ATG AAA      912

Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys
    290                 295                 300

GAA GTC GAA GCG GTT GTT GTT GCT GCC CTC TCA GGG AAA AGT TCG GGT      960

Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly
305                 310                 315                 320

TCC GCA AAA TTG GAA ACA CCT GAG CTC CCC AAG CCC GGG GTG ACA CCA     1008

Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro
                325                 330                 335

AGA TCA GAG GTT ATC GAA ATC GGA CTC GCG CTT GCT AAA GCA ATT CAG     1056

Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln
            340                 345                 350

ACA TTG GGA GAA GCC ACA AAA TCT GCC TTA TCT AAC TAT GCA AGT ACA     1104
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Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr
        355                 360                 365

CAA GCA CAA GCA GAC CAA ACA AAT AAA CTA GGT CTA GAA AAG CAA GCG    1152

Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala
    370                 375                 380

ATA AAA ATC GAT AAA GAA CGA GAA GAA TAC CAA GAG ATG AAG GCT GCC    1200

Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala
385                 390                 395                 400

GAA CAG AAG TCT AAA GAT CTC GAA GGA ACA ATG GAT ACT GTC AAT ACT    1248

Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr
                405                 410                 415

GTG ATG ATC GCG AAG GGG TTC GAA TTG CCA TGG GGG CCC TTA ATT AAT    1296

Val Met Ile Ala Lys Gly Phe Glu Leu Pro Trp Gly Pro Leu Ile Asn
            420                 425                 430     432
```

INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AGCTGTCTGG CAACGAAACG 20

INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCAGCAACAA CAACCGCTTC 20

INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GATCCTGATG TCTATTTCAT CTTCTTCAG 29

INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GTCCTGAAGA AGATGAAATA GACATCAG 28

INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AATTGCCATG GGGGCCCTTA ATTAATTAAC 30

INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TCGAGTTAAT TAATTAAGGG CCCCCATGGC 30

INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:5438 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(ii) MOLECULE TYPE: Other nucleic acid; Plasmid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ATCGATGTTA ACAGATCTAA GCTTAACTAA CTAACTCCGG AAAAGGAGGA ACTTCCATGA 60

TCAGTCTGAT TGCGGCGTTA GCGGTAGATC GCGTTATCGG CATGGAAAAC GCCATGCCGT 120

GGAACCTGCC TGCCGATCTC GCCTGGTTTA AACGCAACAC CTTAAATAAA CCCGTGATTA 180

TGGGCCGCCA TACCTGGGAA TCAATCGGTC GTCCGTTGCC AGGACGCAAA AATATTATCC 240

TCAGCAGTCA ACCGGGTACG GACGATCGCG TAACGTGGGT GAAGTCGGTG GATGAAGCCA 300

TCGCGGCGTG TGGTGACGTA CCAGAAATCA TGGTGATTGG CGGCGGTCGC GTTTATGAAC 360

AGTTCTTGCC AAAAGCGCAA AAACTGTATC TGACGCATAT CGACGCAGAA GTGGAAGGCG 420

ACACCCATTT CCCGGATTAC GAGCCGGATG ACTGGGAATC GGTATTCAGC GAATTCCACG 480

ATGCTGATGC GCAGAACTCT CACAGCTATG AGTTCGAAAT TCTGGAGCGG CGGATCCTGA 540

TGTCTATTTC ATCTTCTTCA GGACCTGACA ATCAAAAAAA TATCATGTCT CAAGTTCTGA 600

CATCGACACC CCAGGGCGTG CCCCAACAAG ATAAGCTGTC TGGCAACGAA ACGAAGCAAA 660

TACAGCAAAC ACGTCAGGGT AAAAACACTG AGATGGAAAG CGATGCCACT ATTGCTGGTG 720

CTTCTGGAAA AGACAAAACT TCCTCGACTA CAAAAACAGA AACAGCTCCA CAACAGGGAG 780

TTGCTGCTGG GAAAGAATCC TCAGAAAGTC AAAAGGCAGG TGCTGATACT GGAGTATCAG 840

GAGCGGCTGC TACTACAGCA TCAAATACTG CAACAAAAAT TGCTATGCAG ACCTCTATTG 900

AAGAGGCGAG CAAAAGTATG GAGTCTACCT TAGAGTCACT TCAAAGCCTC AGTGCCGCGC 960

AAATGAAAGA AGTCGAAGCG GTTGTTGTTG CTGCCCTCTC AGGGAAAAGT TCGGGTTCCG 1020

CAAAATTGGA AACACCTGAG CTCCCCAAGC CCGGGGTGAC ACCAAGATCA GAGGTTATCG 1080

AAATCGGACT CGCGCTTGCT AAAGCAATTC AGACATTGGG AGAAGCCACA AAATCTGCCT 1140

TATCTAACTA TGCAAGTACA CAAGCACAAG CAGACCAAAC AAATAAACTA GGTCTAGAAA 1200

AGCAAGCGAT AAAAATCGAT AAAGAACGAG AAGAATACCA AGAGATGAAG GCTGCCGAAC 1260

AGAAGTCTAA AGATCTCGAA GGAACAATGG ATACTGTCAA TACTGTGATG ATCGCGAAGG 1320

GGTTCGAATT GCCATGGGGG CCCTTAATTA ATTAACTCGA GAGATCCAGA TCTAATCGAT 1380

GATCCTCTAC GCCGGACGCA TCGTGGCCGG CATCACCGGC GCCACAGGTG CGGTTGCTGG 1440

CGCCTATATC GCCGACATCA CCGATGGGGA AGATCGGGCT CGCCACTTCG GGCTCATGAG 1500

CGCTTGTTTC GGCGTGGGTA TGGTGGCAGG CCCGTGGCCG GGGGACTGTT GGGCGCCATC 1560

TCCTTGCATG CACCATTCCT TGCGGCGGCG GTGCTCAACG GCCTCAACCT ACTACTGGGC 1620

TGCTTCCTAA TGCAGGAGTC GCATAAGGGA GAGCGTCGAC CGATGCCCTT GAGAGCCTTC 1680

AACCCAGTCA GCTCCTTCCG GTGGGCGCGG GGCATGACTA TCGTCGCCGC ACTTATGACT 1740

GTCTTCTTTA TCATGCAACT CGTAGGACAG GTGCCGGCAG CGCTCTGGGT CATTTTCGGC 1800

GAGGACCGCT TTCGCTGGAG CGCGACGATG ATCGGCCTGT CGCTTGCGGT ATTCGGAATC 1860

TTGCACGCCC TCGCTCAAGC CTTCGTCACT GGTCCCGCCA CCAAACGTTT CGGCGAGAAG 1920

CAGGCCATTA TCGCCGGCAT GGCGGCCGAC GCGCTGGGCT ACGTCTTGCT GGCGTTCGCG 1980

ACGCGAGGCT GGATGGCCTT CCCCATTATG ATTCTTCTCG CTTCCGGCGG CATCGGGATG 2040

CCCGCGTTGC AGGCCATGCT GTCCAGGCAG GTAGATGACG ACCATCAGGG ACAGCTTCAA 2100

GGATCGCTCG CGGCTCTTAC CAGCCTAACT TCGATCACTG GACCGCTGAT CGTCACGGCG 2160

ATTTATGCCG CCTCGGCGAG CACATGGAAC GGGTTGGCAT GGATTGTAGG CGCCGCCCTA 2220

TACCTTGTCT GCCTCCCCGC GTTGCGTCGC GGTGCATGGA GCCGGGCCAC CTCGACCTGA 2280

ATGGAAGCCG GCGGCACCTC GCTAACGGAT TCACCACTCC AAGAATTGGA GCCAATCAAT 2340

TCTTGCGGAG AACTGTGAAT GCGCAAACCA ACCCTTGGCA GAACATATCC ATCGCGTCCG 2400

CCATCTCCAG CAGCCGCACG CGGCGCATCT CGGGCAGCGT TGGGTCCTGG CCACGGGTGC 2460

GCATGATCGT GCTCCTGTCG TTGAGGACCC GGCTAGGCTG GCGGGGTTGC CTTACTGGTT 2520

AGCAGAATGA ATCACCGATA CGCGAGCGAA CGTGAAGCGA CTGCTGCTGC AAAACGTCTG 2580

CGACCTGAGC AACAACATGA ATGGTCTTCG GTTTCCGTGT TTCGTAAAGT CTGGAAACGC 2640

GGAAGTCAGC GCCCTGCACC ATTATGTTCC GGATCTGCAT CGCAGGATGC TGCTGGCTAC 2700

CCTGTGGAAC ACCTACATCT GTATTAACGA AGCGCTGGCA TTGACCCTGA GTGATTTTTC 2760

TCTGGTCCCG CCGCATCCAT ACCGCCAGTT GTTTACCCTC ACAACGTTCC AGTAACCGGG 2820

CATGTTCATC ATCAGTAACC CGTATCGTGA GCATCCTCTC TCGTTTCATC GGTATCATTA 2880

CCCCCATGAA CAGAAATTCC CCCTTACACG GAGGCATCAA GTGACCAAAC AGGAAAAAAC 2940

CGCCCTTAAC ATGGCCCGCT TTATCAGAAG CCAGACATTA ACGCTTCTGG AGAAACTCAA 3000

CGAGCTGGAC GCGGATGAAC AGGCAGACAT CTGTGAATCG CTTCACGACC ACGCTGATGA 3060

GCTTTACCGC AGCTGCCTCG CGCGTTTCGG TGATGACGGT GAAAACCTCT GACACATGCA 3120

GCTCCCGGAG ACGGTCACAG CTTGTCTGTA AGCGGATGCC GGGAGCAGAC AAGCCCGTCA 3180

GGGCGCGTCA GCGGGTGTTG GCGGGTGTCG GGGCGCAGCC ATGACCCAGT CACGTAGCGA 3240

TAGCGGAGTG TATACTGGCT TAACTATGCG GCATCAGAGC AGATTGTACT GAGAGTGCAC 3300

CATATGCGGT GTGAAATACC GCACAGATGC GTAAGGAGAA AATACCGCAT CAGGCGCTCT 3360

TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC GGCTGCGGCG AGCGGTATCA 3420

GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG GGGATAACGC AGGAAAGAAC 3480

ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT 3540

TTCCATAGGC TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG 3600

CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC CCTCGTGCGC 3660

TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG CCTTTCTCCC TTCGGGAAGC 3720

GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT CGGTGTAGGT CGTTCGCTCC 3780

AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC 3840

TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC AGCCACTGGT 3900

AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA GTGGTGGCCT 3960

AACTACGGCT ACACTAGAAG GACAGTATTT GGTATCTGCG CTCTGCTGAA GCCAGTTACC 4020

TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA CCACCGCTGG TAGCGGTGGT 4080

TTTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAAG GATCTCAAGA AGATCCTTTG 4140

ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG GATTTTGGTC 4200

ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA ATTAAAAATG AAGTTTTAAA 4260

TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG 4320

GCACCTATCT CAGCGATCTG TCTATTTCGT TCATCCATAG TTGCCTGACT CCCCGTCGTG 4380

TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA 4440

GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG 4500

CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG TTGCCGGGAA 4560

GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG TTGTTGCCAT TGCTGCAGGC 4620

ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTTC CCAACGATCA 4680

AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCCTCCG 4740

ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT 4800

AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGACTGGTGA GTACTCAACC 4860

AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT CTTGCCCGGC GTCAACACGG 4920

GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA ACGTTCTTCG 4980

GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT 5040

GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAACA 5100

GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG AATACTCATA 5160

CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT ATTGTCTCAT GAGCGGATAC 5220

ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC CGCGCACATT TCCCCGAAAA 5280

GTGCCACCTG ACGTCTAAGA AACCATTATT ATCATGACAT TAACCTATAA AAATAGGCGT 5340

ATCACGAGGC CCTTTCGTCT TCAAGAATTA ATTGTTATCC GCTCACAATT AATTCTTGAC 5400

AATTAGTTAA CTATTTGTTA TAATGTATTC ATAAGCTT 5438

INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GCTGCCGAAC AGAAGTCTAA 20

INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CTCGAAGGAA CAATGGATAC 20

INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GTACATATTG TCGTTAGAAC GCG 23

INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TAATACGACT CACTATAGGG AGA 23

INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GCGGATCCTG ATGTCTATTT CATCTTCT 28

INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: Other nucleic acid; Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATCTCGAGTT TTATGCTGCT GCGCCAGCGA 30

Claims

1. A Chlamydia pneumoniae antigenic polypeptide, which comprises polypeptide A containing a sequence of at least 5 consecutive amino acids in the polypeptide of SEQ ID NO: 1.

2. The antigenic polypeptide of claim 1, wherein said polypeptide A is a polypeptide in which at least one amino acid is deleted from the polypeptide of SEQ ID NO: 1.

3. The antigenic polypeptide of claim 1, wherein said polypeptide A is a polypeptide in which at least one amino acid in the polypeptide of SEQ ID NO: 1 is replaced with other amino acid or a polypeptide in which at least one amino acid is added in the polypeptide of SEQ ID NO: 1.

4. The antigenic polypeptide of claim 1, wherein said polypeptide A is a polypeptide in which an amino acid or a peptide sequence is bound to a sequence of at least 5 consecutive amino acids in the polypeptide of SEQ ID NO: 1.

5. The antigenic polypeptide of claim 1, wherein said polypeptide A is a polypeptide containing the amino acid sequence of SEQ ID NO: 1.

6. The antigenic polypeptide of claim 1, wherein said polypeptide A is a polypeptide containing the amino acid sequence of SEQ ID NO: 2.

7. The antigenic polypeptide of claim 1, wherein said polypeptide A is a polypeptide containing the amino acid sequence of SEQ ID NO: 5.

8. A DNA encoding the antigenic polypeptide of any one of claims 1-7, or a DNA complementary thereto.

9. The DNA of claim 8, which contains the base sequence of SEQ ID NO: 3.

10. The DNA of claim 8, which contains the base sequence of SEQ ID NO: 4.

11. The DNA of claim 8, which contains the base sequence of SEQ ID NO: 7.

12. A recombinant vector carrying the DNA of any one of claims 8-11.

13. The recombinant vector of claim 12, which is plasmid pCPN533 α containing the base sequence of SEQ ID NO: 10.

14. A transformant containing the recombinant vector of claim 12 or 13.

15. A method for production of an anti-Chlamydia pneumoniae antibody, wherein the antigenic polypeptide of any one of claims 1-7 is used as an antigen.

16. A method for detection and/or measurement of an anti-Chlamydia pneumoniae antibody, wherein the antigenic polypeptide of any one of claims 1-7 is used as an antigen.

17. A reagent for detection and/or measurement of an anti-Chlamydia pneumoniae antibody, which comprises the antigenic polypeptide of any one of claims 1-7 as an antigen.

18. A reagent for diagnosis of a Chlamydia pneumoniae infection, which comprises the antigenic polypeptide of any one of claims 1-7 as an active ingredient.

19. A fused protein of a Chlamydia pneumoniae antigenic polypeptide with dihydrofolate reductase, in which polypeptide B containing a sequence of at least 5 consecutive amino acids in the polypeptide of SEQ ID NO: 1 is bound to the polypeptide of SEQ ID NO: 14 either directly or via an intervening amino acid or amino acid sequence.

20. The fused protein of claim 19, wherein said polypeptide B is a polypeptide in which at least one amino acid is deleted from the polypeptide of SEQ ID NO: 1.

21. The fused protein of claim 19, wherein said polypeptide B is a polypeptide in which at least one amino acid in the polypeptide of SEQ ID NO: 1 is replaced with other amino acids or a polypeptide in which at least one amino acid is added in the polypeptide of SEQ ID NO: 1.

22. The fused protein of claim 19, which is a polypeptide containing the amino acid sequence of SEQ ID NO: 15.

23. The fused protein of claim 19, which is a polypeptide containing the amino acid sequence of SEQ ID NO: 16.

24. A DNA encoding the fused protein of any one of claims 19-23, or a DNA complementary thereto.

25. The DNA of claim 24, which contains the base sequence of SEQ ID NO: 17.

26. The DNA of claim 24, which contains the base sequence of SEQ ID NO: 18.

27. A recombinant vector carrying the DNA of any one of claims 24-26.

28. The recombinant vector of claim 27, which is plasmid pCPN533T.

29. A transformant containing the recombinant vector of claim 27 or 28.

30. A method for production of an anti-Chlamydia pneumoniae antibody, wherein the fused protein of any one of claims 19-23 is used as an antigen.

31. A method for detection and/or measurement of an anti-Chlamydia pneumoniae antibody, wherein the fused protein of any one of claims 19-23 is used as an antigen.

32. A reagent for detection and/or measurement of an anti-Chlamydia pneumoniae antibody, which comprises the fused protein of any one of claims 19-23 as an antigen.

33. A reagent for diagnosis of a Chlamydia pneumoniae infection, which comprises the fused protein of any one of claims 19-23 as an active ingredient.

34. A probe for detection and/or measurement of Chlamydia pneumoniae gene, which comprises any one of

(a) a DNA containing a sequence of at least 10 consecutive bases in the DNA of SEQ ID NO: 3,
(b) a DNA complementary to DNA (a), or
(c) a DNA having at least 90% homology to DNA (a) or (b).

35. The probe of claim 34, which contains the base sequence of SEQ ID NO: 19.

36. The probe of claim 34, which contains the base sequence of SEQ ID NO: 20.

37. A method for detection and/or measurement of Chlamydia pneumoniae gene, wherein the probe of any one of

claims 34-36 is used.

38. A reagent for detection and/or measurement of Chlamydia pneumoniae gene, which comprises the probe of any one of claims 34-36.

39. A reagent for diagnosis of a Chlamydia pneumoniae infection, which comprises the probe of any one of claims 34-36 as an active ingredient.

40. A primer for detection and/or measurement of Chlamydia pneumoniae gene, which comprises any one of

(a) a DNA containing a sequence of at least 10 consecutive bases in the DNA of SEQ ID NO: 3,
(b) a DNA complementary to DNA (a), or
(c) a DNA having at least 90% homology to DNA (a) or (b).

41. The primer of claim 40, which contains the base sequence of SEQ ID NO: 19.

42. The primer of claim 40, which contains the base sequence of SEQ ID NO: 20.

43. A method for detection and/or measurement of Chlamydia pneumoniae gene, wherein the primer of any one of claims 40-42 is used.

44. A reagent for detection and/or measurement of Chlamydia pneumoniae gene, which comprises the primer of any one of claims 40-42.

45. A reagent for diagnosis of a Chlamydia pneumoniae infection, which comprises the primer of any one of claims 40-42 as an active ingredient.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP95/01896

A. CLASSIFICATION OF SUBJECT MATTER
Int. Cl[6] C07K14/295, C12N15/31, C12N1/21, C12P21/02, C12P21/08, C12Q1/68, G01N33/569
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
Int. Cl[6] C07K14/295, C12N15/31, C12N1/21, C12P21/02, C12P21/08, C12Q1/68, G01N33/569

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
CAS ONLINE, WPI, WPI/L, BIOSIS PREVIEWS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	KIKUTA L. C. et al., "Isolation and Sequence Analysis of the Chlamydia pneumoniae GroE Operon" INFECTION AND IMMUNITY, Dec. 1991, Vol. 59, No. 12, pages 4665-4669	1 - 15, 19 - 30
A	KORNAK J. M. et al., "Sequence Analysis of the Gene Encoding the Chlamydia pneumoniae DnaK Protein Homolog" INFECTION AND IMMUNITY, Feb. 1991, Vol. 59, No. 2, pages 721-725	1 - 14, 19 - 29
A	MELGOSA M. P. et al., "Sequence Analysis of the Major Outer membrane Protein Gene of Chlamydia pneumoniae" INFECTION AND IMMUNITY, Jun. 1991, Vol. 59, No. 6, pages 2195-2199	1 - 14, 19 - 29
A	JP, 4-297871, A (Hitachi Chemical Co., Ltd.), October 21, 1992 (21. 10. 92) & EP, 456524, A1 & US, 5318892, A	16 - 18, 31 - 33
A	JP, 5-317097, A (Fuso Pharmaceutical Co., Ltd.),	34 - 45

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
December 8, 1995 (08. 12. 95)	December 26, 1995 (26. 12. 95)
Name and mailing address of the ISA/ Japanese Patent Office	Authorized officer
Facsimile No.	Telephone No.

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP95/01896

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	December 3, 1993 (03. 12. 93) & EP, 402993, A1 & CA, 2017520, A & FI, 9002990, A & US, 5085986, A & KR, 9209424, B1	

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